



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 163666

TO: John Ulm
Location: rem/4E79/4C70
Art Unit: 1649

Sept. 1, 2005

Case Serial Number: 10/719692

From: P. Sheppard
Location: Remsen Building
Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes

THIS PAGE BLANK (USPTO)

STIC-Biotech/ChemLib

163 666

Me

From: Ulm, John
Sent: Wednesday, August 24, 2005 9:58 AM
To: STIC-Biotech/ChemLib
Subject: search SEQ ID NO:6 of application Serial Number 10/719,692

Please search SEQ ID NO:6 of application Serial Number 10/719,692.
John Ulm. 571 272-0880, Room REM 4E79, mail box REM 4C70, results preferred in paper.

Thank you.

RECEIVED
AUG 24 2005
STIC

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2005, 18:20:50 ; Search time 166 Seconds
(without alignments)
806.139 Million cell updates/sec

Title: US-10-719-692-6
Perfect score: 1853
Sequence: 1 MTNGSCCRIGDTISQVMP...ANFSQSQDQWDPHVEMH 346

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1853	100.0	346	4	AAG80968 Human nGP
2	1853	100.0	346	4	ABBA4522 Human GPC
3	1853	100.0	346	4	AAU06197 Novel hum
4	1853	100.0	346	4	AAU04373 Human G-p
5	1853	100.0	346	5	AAE16172 Human G-p
6	1853	100.0	346	5	AAU11401 HM74-like
7	1853	100.0	346	5	AAE17077 Human G-p
8	1853	100.0	346	5	ABBO8596 Human lip
9	1853	100.0	346	5	ABG93786 Human G D
10	1853	100.0	346	5	ABP95599 Human GPC
11	1853	100.0	346	5	AAO14788 Human pur
12	1853	100.0	346	5	AAE24354 Human G p
13	1853	100.0	346	6	ABP81747 Human che
14	1853	100.0	346	6	ABP56751 Human GAV
15	1853	100.0	346	6	AAO26511 Human G-P
16	1853	100.0	346	6	ABP58453 Human res
17	1853	100.0	346	7	ADC46872 Human TA-
18	1853	100.0	346	7	ABW00810 Human GPC
19	1853	100.0	346	7	ADE40282 Human NOV
20	1853	100.0	346	7	ADE40272 Human NOV
21	1853	100.0	346	7	ADE40278 Human NOV
22	1853	100.0	346	7	ABW02123 Human GPC
23	1853	100.0	346	7	ADI21235 Novel hum
24	1853	100.0	346	7	ADL96470 Human G p
25	1853	100.0	346	8	ADJ71681 Human NOV

26	1853	100.0	346	8	ADJ71689	Adj71689 Human NOV
27	1853	100.0	346	8	ADJ71677	Adj71677 Human NOV
28	1853	100.0	346	8	ADM46116	Adm46116 Human 5-o
29	1853	100.0	346	8	ADO29444	Ado29444 Human GPC
30	1853	100.0	346	8	ADT08049	Adt08049 Human che
31	1853	100.0	352	7	ADF40286	Ade40286 Human NOV
32	1853	100.0	584	7	ADF70465	Adf70465 Orphan re
33	1849	99.8	346	6	ABB82502	ABb82502 Human TGR
34	1848	99.7	345	8	ADJ71693	Adj71693 Human NOV
35	1846	99.6	346	7	ADE40274	Ade40274 Human NOV
36	1846	99.6	346	8	ADJ71683	Adj71683 Human NOV
37	1839	99.2	346	4	ABB44523	Abb44523 Human GPC
38	1839	99.2	346	7	ADE40276	Ade40276 Human NOV
39	1839	99.2	346	7	ABW02124	Abw02124 Human GPC
40	1839	99.2	346	8	ADJ71685	Adj71685 Human NOV
41	1739	93.8	342	5	ABP54312	Abp54312 Human G p
42	1686	91.0	314	7	ADE40280	Ade40280 Human NOV
43	1686	91.0	314	8	ADJ71687	Adj71687 Human NOV
44	1686	91.0	320	7	ADE40288	Ade40288 Human NOV
45	1686	91.0	320	7	ADE40284	Ade40284 Human NOV

ALIGNMENTS

RESULT 1

AAG80968

ID AAG80968 standard; protein; 346 AA.

XX AAG80968;

XX DT 28-AUG-2001 (first entry)

XX DE Human nGPCr11 #2.

XX KW G protein-coupled receptor; nGPCR; seven transmembrane receptor;
signal transduction; schizophrenia; thyroid disorder; renal failure;
rheumatoid arthritis; CNS disorder; infection; metabolic disease;
cardiovascular disease; proliferative disorder; hormonal disorder;
neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
attention deficit-hyperactivity disorder/attention deficit disorder;
Parkinson's disease; migraine; senile dementia; inflammatory disease;
rheumatoid arthritis; autoimmune disorder; respiratory ailment;

XX OS Homo sapiens.

XX PN WO200136473-A2.

XX PD 25-MAY-2001.

XX PF 16-NOV-2000; 2000WO-US031581.

XX PR 16-NOV-1999; 99US-0165838P.

XX PR 17-NOV-1999; 99US-0166071P.

XX PR 19-NOV-1999; 99US-0166678P.

XX PR 28-DEC-1999; 99US-0173396P.

XX PR 22-FEB-2000; 2000US-0184129P.

XX PR 28-FEB-2000; 2000US-0185421P.

XX PR 28-FEB-2000; 2000US-0185554P.

XX PR 02-MAR-2000; 2000US-0186530P.

XX PR 03-MAR-2000; 2000US-0186811P.

XX PR 09-MAR-2000; 2000US-0188114P.

XX PR 17-MAR-2000; 2000US-0190310P.

XX PR 21-MAR-2000; 2000US-0190800P.

XX PR 20-APR-2000; 2000US-0198568P.

XX PR 02-MAY-2000; 2000US-0201190P.

XX PR 08-MAY-2000; 2000US-0203111P.

XX PR 25-MAY-2000; 2000US-0207094P.

XX (PHAA) PHARMACIA & UPJOHN CO.

PA Vogeli G, Wood LS, Parodi LA, Hiesch RR, Lind P, Slightom J;

PI

PI Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
XX WPI; 2001-389826/41.
DR N-PSDB; AAH51008.
XX
XX New G protein-coupled receptor (ngPCR-x) and its encoding polynucleotide
PT useful for diagnosing and treating e.g. schizophrenia.
XX
XX Claim 37; Page 89; 261pp; English.
XX
XX The present invention relates to novel G protein-coupled receptors
CC (ngPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28,
CC 31-38, 40, 41, 53-60) and their coding sequences. The present sequence is
CC one such G protein-coupled receptor. GPCRxs are also known as seven
CC transmembrane receptors and function in signal transduction. The ngPCRx
CC coding sequences are useful for screening a human to diagnose a disorder
CC affecting the brain or a genetic predisposition, specifically
CC schizophrenia. ngPCRx are useful for identifying compounds useful for
CC treating schizophrenia. Detection of ngPCRx in a sample is useful as a
CC diagnostic tool for diseases or disorders e.g. thyroid disorders, renal
CC failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1,
CC metabolic and cardiovascular diseases, proliferative disorders and
CC hormonal disorders. Modulators of ngPCRx activity have the utility for
CC treating neurological disorders, including schizophrenia, ADHD/ADD
CC (attention deficit-hyperactivity disorder/attention deficit disorder),
CC and neuronal disorders such as Alzheimer's disease, Parkinson's disease,
CC migraine and senile dementia. Additional disorders include inflammatory
CC conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune
CC disorders, cancers, respiratory ailments such as asthma, and inflammatory
CC diseases e.g. inflammatory bowel disease
XX
SQ Sequence 346 AA;
Query Match 100.0%; Score 1853; DB 4; Length 346;
Best Local Similarity 100.0%; Pred. No. 7, 4e-199;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYNGSCRIEGDTISQVMPPLIIVFVLGALNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
DB 1 MYNGSCRIEGDTISQVMPPLIIVFVLGALNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
QY 61 DFLMLTCLPRTDYLLRRHAFGDI PCRVGLFTLAMNAGSIVFTVVAADRYPKVHP 120
DB 61 DFLMLTCLPRTDYLLRRHAFGDI PCRVGLFTLAMNAGSIVFTVVAADRYPKVHP 120
QY 121 HVAVNTISRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180
DB 121 HVAVNTISRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180
QY 181 FOLEFPMPLGIILFCSFKIWSLRRRQQLARQARKKATRFIMVAIVITCYLPSVSAR 240
DB 181 FOLEFPMPLGIILFCSFKIWSLRRRQQLARQARKKATRFIMVAIVITCYLPSVSAR 240
QY 241 LYFLMTVPSSACDPSVHGALHTLTSTYNNMMLDPLVYVFPSSPKPKFKYKLIKICSLKPK 300
DB 241 LYFLMTVPSSACDPSVHGALHTLTSTYNNMMLDPLVYVFPSSPKPKFKYKLIKICSLKPK 300
QY 301 QPGHKTQRPPEMPISNLGRRCISVANSFQSQDQMDPHIVEWH 346
DB 301 QPGHKTQRPPEMPISNLGRRCISVANSFQSQDQMDPHIVEWH 346
RESULT 2
ID ABB44522
XX ID ABB44522 standard; protein; 346 AA.
AC ABB44522;
XX
XX 28-JAN-2002 (first entry)
XX
XX Human GPCR1a polypeptide SEQ ID NO 2.
XX
XX Human; GPCR; G-coupled protein-receptor; cardiant; antiarteriosclerotic;

KW anabolic; cytostatic; antiviral; gene therapy; cardiomyopathy; obesity;
KW anorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis;
KW asthma; Alzheimer's disease; Parkinson's disorder; Huntington's disease;
KW infection; human immunodeficiency virus; HIV.
XX Homo sapiens.
XX WO200174904-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US010241.
XX 31-MAR-2000; 2000US-0193664P.
XX 05-APR-2000; 2000US-0194614P.
XX 06-APR-2000; 2000US-0195063P.
XX 06-APR-2000; 2000US-0195066P.
XX 06-APR-2000; 2000US-0195067P.
XX 06-APR-2000; 2000US-0195068P.
XX 06-APR-2000; 2000US-0195069P.
XX 06-APR-2000; 2000US-0195070P.
XX 06-APR-2000; 2000US-0195510P.
XX 21-JUL-2000; 2000US-0219855P.
XX 27-JUL-2000; 2000US-0221284P.
XX 28-JUL-2000; 2000US-0221325P.
XX 11-AUG-2000; 2000US-0224588P.
XX 11-OCT-2000; 2000US-0239613P.
XX 18-JAN-2001; 2001US-0262508P.
XX 23-JAN-2001; 2001US-0263433P.
XX 23-JAN-2001; 2001US-0263604P.
XX 30-JAN-2001; 2001US-0285161P.
XX 29-MAR-2001; 2001US-00823172.
XX (CURA-) CURAGEN CORP.
XX Majumder K, Vernet CAM, Casman SJ, Wolenc AR, Spaderna SK;
PI Padigaru M, Mishnu VS, Tchernev VT, Spytek KA, Li L, Baumgartner JC;
PI Gusev VY;
XX WPI; 2001-639351/73.
XX N-PSDB; ABA81529, ABA81530.
XX New human G-protein coupled receptor X, GPCRx, polypeptide useful in
PT treatment or prevention of GPCRx associated disorders e.g. cardiomyopathy
PT or atherosclerosis, and to screen for antagonists and agonists useful
PT therapeutically.
XX Claim 1; Page 8; 157pp; English.
XX The invention relates to nucleic acid sequences (ABA81529-ABA81552) that
CC encode G-coupled protein-receptor related polypeptides (ABB44522-
CC ABB44543). The isolated polypeptide having a sequence differing by no
CC more than 15 % of amino acid residues from one of 22 amino acid sequences
CC (or mature forms of the sequences), fully defined in the specification
CC and corresponding to human G-protein coupled receptor X (GPCRX)
CC polypeptides. The polypeptides have potential cardiant,
CC antiarteriosclerotic, anabolic, cytostatic and antiviral activity. The
CC polypeptides can be administered therapeutically, especially using gene
CC therapy and expressing the encoding DNA in vivo, to treat or prevent
CC GPCRx-associated disorders, especially in humans. For example, they can
CC be used to treat/prevent cardiomyopathy, atherosclerosis, disorders
CC related to signal processing and metabolic pathway modulation (e.g.
CC obesity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple
CC sclerosis, asthma, cancers, neurodegenerative disorders (e.g. Alzheimer's
CC disease, Parkinson's disorder, Huntington's disease), immune disorders,
CC haematopoietic disorders, developmental diseases, neurological disorders,
CC bacterial, fungal, protozoal and viral infections (e.g. with human
CC immunodeficiency virus (HIV)-1 or HIV-2). They can be used diagnostically
CC to determine the presence of or predisposition to a disease associated
CC with altered levels of the polypeptide in mammals (especially humans) by
CC detecting alterations in polypeptide expression levels relative to
CC control samples. They are useful to identify agents binding polypeptide
CC (e.g. cellular receptors or downstream effectors) and/or agents

CC modulating cellular polypeptide expression or activity, useful as
 CC antagonists and agonists in disease treatment
 XX Sequence 346 AA;
 SQ

Query Match 100.0%; Score 1853; DB 4; Length 346;
 Best Local Similarity 100.0%; Pred. No. 7.4e-199; Mismatches 0; Indels 0; Gaps 0;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNGSCCRIEGDTISQVMPPLLIIVAFVLGALNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
 DB 1 MYNGSCCRIEGDTISQVMPPLLIIVAFVLGALNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

QY 61 DFLLMICLPFRDYYLRRRHWAFFGDI PCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHP 120
 DB 61 DFLLMICLPFRDYYLRRRHWAFFGDI PCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHP 120

QY 121 HNAVNTISTRVAAGIVCTLMALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180
 DB 121 HNAVNTISTRVAAGIVCTLMALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180

QY 181 FOLEFPMPLGIILFCSFKIVMSLRRLRQQLARQARKKATRFIMVVAIVFITCYLPSVSAR 240
 DB 181 FOLEFPMPLGIILFCSFKIVMSLRRLRQQLARQARKKATRFIMVVAIVFITCYLPSVSAR 240

QY 241 LYFLMTVPSSACDPSVHGALHITLSFTYNSMLDPLVYFFSSPFPKFNKLIKSLKPK 300
 DB 241 LYFLMTVPSSACDPSVHGALHITLSFTYNSMLDPLVYFFSSPFPKFNKLIKSLKPK 300

QY 301 QPGHKTQRPPEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346
 DB 301 QPGHKTQRPPEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346

RESULT 3
 AAU06197
 ID AAU06197 standard; protein; 346 AA.
 AC AAU06197;
 XX
 XX
 XX 19-DEC-2001 (first entry)
 DE Novel human G protein-coupled receptor (GPCR) protein.
 XX
 XX Human; G-protein coupled receptor; GPCR; chemokine receptor; protease;
 KW hyperproliferative disorder; neurological disorder; psychiatric disease;
 KW inflammatory disorder; respiratory disorder.
 XX
 OS Homo sapiens.
 XX
 XX WO200173029-A2.
 XX
 PD 04-OCT-2001.
 XX
 XX 27-MAR-2001; 2001WO-US009522.
 XX
 PR 27-MAR-2000; 2000US-0192419P.
 PR 06-SEP-2000; 2000US-0230459P.
 PR 20-SEP-2000; 2000US-0066653S.
 XX
 XX (PEKE) PE CORP NY.
 PA
 XX
 XX Ye J, Cravchik A, Di Francesco V, Beasley EM;
 PI
 XX WPI; 2001-616503/71.
 DR N-PSDB; AAS12581.
 DR
 XX Novel human G-protein coupled receptor proteins and nucleic acid
 PT molecules encoding the protein for use in developing human therapeutics
 PT and diagnostic compositions and for identifying modulators of the
 PT protein.
 XX
 PS Claim 1; Fig 1; 66pp; English.

XX The present invention relates to the isolation of a novel human G-protein
 CC coupled receptor (GPCR) which is related to the chemokine receptor
 CC subfamily. The cDNA and gene sequences encoding for GPCR are also given
 CC in the invention. The sequences of the invention are useful for
 CC diagnosing and treating diseases or conditions mediated by human
 CC proteases. Such diseases include hyperproliferative disorders (e.g.
 CC hyperplasia), neurological disorders (e.g. Parkinson's disease),
 CC psychiatric diseases (e.g. schizophrenia), inflammatory disorders (e.g.
 CC diabetic) and respiratory disorders (e.g. adult respiratory distress
 CC syndrome, ARDS). The GPCR protein is also useful for identifying a
 CC modulator of the expression of the protein. It also serves as a target
 CC for identifying agents for use in mammalian therapeutic applications,
 CC e.g. a human drug, particularly modulating a biological or pathological
 CC response in a cell or tissue that expresses the protein, in biological
 CC assays related to GPCRs that are related to members of the chemokine
 CC receptor subfamily, in drug screening assays and in competition binding
 CC assays. GPCR is also useful in diagnosing a disease or predisposition to
 CC a disease mediated by the peptide, in pharmacogenomic analysis. The
 CC polynucleotide sequences can also be used in gene therapy. The present
 CC sequence represents the novel human GPCR of the invention
 XX
 SQ Sequence 346 AA;

Query Match 100.0%; Score 1853; DB 4; Length 346;
 Best Local Similarity 100.0%; Pred. No. 7.4e-199;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNGSCCRIEGDTISQVMPPLLIIVAFVLGALNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
 DB 1 MYNGSCCRIEGDTISQVMPPLLIIVAFVLGALNGVALCGFCFHMKTWKPSTVYLFNLAVA 60

QY 61 DFLLMICLPFRDYYLRRRHWAFFGDI PCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHP 120
 DB 61 DFLLMICLPFRDYYLRRRHWAFFGDI PCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHP 120

QY 121 HNAVNTISTRVAAGIVCTLMALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180
 DB 121 HNAVNTISTRVAAGIVCTLMALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180

QY 181 FOLEFPMPLGIILFCSFKIVMSLRRLRQQLARQARKKATRFIMVVAIVFITCYLPSVSAR 240
 DB 181 FOLEFPMPLGIILFCSFKIVMSLRRLRQQLARQARKKATRFIMVVAIVFITCYLPSVSAR 240

QY 241 LYFLMTVPSSACDPSVHGALHITLSFTYNSMLDPLVYFFSSPFPKFNKLIKSLKPK 300
 DB 241 LYFLMTVPSSACDPSVHGALHITLSFTYNSMLDPLVYFFSSPFPKFNKLIKSLKPK 300

QY 301 QPGHKTQRPPEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346
 DB 301 QPGHKTQRPPEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346

RESULT 4
 AAU04373
 ID AAU04373 standard; protein; 346 AA.
 XX
 AC AAU04373;
 XX
 XX 23-OCT-2001 (first entry)
 DT
 XX
 XX Human G-protein coupled receptor, hrUP19.
 DE
 XX Human; G-protein coupled receptor; GPCR; hrUP19; agonist;
 KW inverse agonist; lung cancer.
 XX
 OS Homo sapiens.
 XX
 XX WO200136471-A2.
 EN
 XX 25-MAY-2001.
 PD
 XX 16-NOV-2000; 2000WO-US031509.

```
XX 17-NOV-1999; 99US-0166088P.
PR 17-NOV-1999; 99US-0166099P.
PR 17-NOV-1999; 99US-0166369P.
PR 23-DEC-1999; 99US-0171900P.
PR 23-DEC-1999; 99US-0171901P.
PR 23-DEC-1999; 99US-0171902P.
PR 11-FEB-2000; 2000US-0181749P.
PR 14-MAR-2000; 2000US-0189258P.
PR 14-MAR-2000; 2000US-0189259P.
PR 10-APR-2000; 2000US-0195898P.
PR 10-APR-2000; 2000US-0195899P.
PR 10-APR-2000; 2000US-0196078P.
PR 28-APR-2000; 2000US-0200419P.
PR 12-MAY-2000; 2000US-0203630P.
PR 12-JUN-2000; 2000US-0210741P.
PR 12-JUN-2000; 2000US-0210982P.
PR 21-AUG-2000; 2000US-0226760P.
PR 26-SEP-2000; 2000US-0235418P.
PR 26-SEP-2000; 2000US-0235779P.
PR 20-OCT-2000; 2000US-0243332P.
PR 20-OCT-2000; 2000US-0243343P.
PR 24-OCT-2000; 2000US-0243019P.
XX (AREN-) ARENA PHARM INC.
XX
XX Chen R, Dang HT, Lowitz KP;
PI WPI; 2001-355616/37.
XX N-PSDB; AAS07946.
XX
PT Endogenous and non-endogenous versions of human G-protein coupled
PT receptors for direct identification of candidate compounds as agonists,
PT inverse agonists or partial agonists for use as therapeutic agents.
XX
XX Claim 45; Page 110-111; 160pp; English.
XX
XX The sequence represents a human G-protein coupled receptor (GPCR),
CC hRUP19. The endogenous and non-endogenous, constitutively activated
CC versions of human G-protein coupled receptors (GPCR), are useful for
CC direct identification of candidate compounds as receptor agonists,
CC inverse agonists or partial agonists having applicability as therapeutic
CC agents for treating diseases related to GPCR, e.g. lung cancer. Non-
CC endogenous version of human GPCRs are also utilized in research settings
CC and in vitro and in vivo system, incorporating GPCRs can be utilised to
CC elucidate and understand the roles these receptors play in the human
CC condition, both normal and diseased
XX
XX Sequence 346 AA;
SQ
Query Match 100.0%; Score 1853; DB 4; Length 346;
Best Local Similarity 100.0%; Pred. No. 7.4e-199;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYNGSCRIEGTTSIQVMPPLIIVAFVLGALNGVALCGFCFHMKTWKBSTVYLFNLVA 60
DB 1 MYNGSCRIEGTTSIQVMPPLIIVAFVLGALNGVALCGFCFHMKTWKBSTVYLFNLVA 60
QY 61 DELLMLICLPFRDYYLRRRHAFGDIICRVGLFTLANNRAGSIVFLTVVAADRYFKVHP 120
DB 61 DELLMLICLPFRDYYLRRRHAFGDIICRVGLFTLANNRAGSIVFLTVVAADRYFKVHP 120
QY 121 HVAVNTISTRVAGIVCTIWAIVLGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180
DB 121 HVAVNTISTRVAGIVCTIWAIVLGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180
QY 181 FOLEFPMPIGILFCSFKIWSLRRRQOLARQARKKATRFIMVAIVFITCYLPSVSAR 240
DB 181 FOLEFPMPIGILFCSFKIWSLRRRQOLARQARKKATRFIMVAIVFITCYLPSVSAR 240
QY 241 LYFLWTVPSSACDPSVHGALHITLSFTYNSMLDPLVYFFSSPFPKFNKLIKICSLKPK 300
DB 241 LYFLWTVPSSACDPSVHGALHITLSFTYNSMLDPLVYFFSSPFPKFNKLIKICSLKPK 300
```

```
QY 301 QPGHSKTQRPPEMPISNLGRSCISVANSFOSQSDGQWDPHIVEWH 346
DB 301 QPGHSKTQRPPEMPISNLGRSCISVANSFOSQSDGQWDPHIVEWH 346

RESULT 5
AAE16172
ID AAE16172 standard; protein; 346 AA.
XX
XX AAE16172;
XX
XX 26-MAR-2002 (first entry)
XX
XX Human G-protein coupled receptor 3 (GCRC-3) protein.
XX
XX Human; G-protein coupled receptor 3; cell proliferative disorder;
XX arteriosclerosis; hepatitis; cancer; neurological disorder; epilepsy;
XX Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
XX atherosclerosis; hypertension; myocardial infarction; peptic ulcer;
XX gastrointestinal disorder; dysphagia; anorexia; autoimmune disorder;
XX acquired immune deficiency syndrome; inflammatory disorder; infection;
XX Addison's disease; allergy; Grave's disease; metabolic disorder; AIDS;
XX diabetes; obesity; osteoporosis; gene therapy; GCRC-3.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..32
XX /label= Signal_peptide
XX Domain 20..44
XX /note= "Transmembrane domain"
XX FT Protein 33..346
XX /label= Human_mature_GCRC-3_protein
XX FT Domain 93..110
XX /note= "Transmembrane domain"
XX FT Domain 137..154
XX /note= "Transmembrane domain"
XX FT Domain 222..244
XX /note= "Transmembrane domain"
XX
XX WO200187937-A2.
XX
XX 22-NOV-2001.
XX
XX 17-MAY-2001; 2001WO-US016285.
XX
XX 18-MAY-2000; 2000US-0205628P.
XX 22-MAY-2000; 2000US-0206222P.
XX 25-MAY-2000; 2000US-0207566P.
XX 02-JUN-2000; 2000US-0208834P.
XX 02-JUN-2000; 2000US-0208861P.
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Patterson C, Lu DAM, Thornton M, Lu Y, Tribouley CM, Graul R;
XX Khan FA, Gandhi AR, Wallia NK, Nguyen DB, Yue H, Hafalia A;
XX Elliott VS, Lal P, Reddy R, Kallick DA, Tang TY, Au-Young J;
XX WPI; 2002-089844/12.
XX
XX N-PSDB; AAD26371.
XX
XX Novel G-protein coupled receptors and polynucleotides useful for
XX diagnosis, treatment and prevention of disorders of cell proliferation,
XX neurological, cardiovascular, metabolic disorders and viral infections.
XX
XX Claim 1; Page 105-106; 115pp; English.
XX
XX The invention relates to human G-protein coupled receptor (GCRC)
XX polypeptides and polynucleotides. GCRC polypeptides are useful for
XX screening compounds that modulate their activity. They are useful in the
XX diagnosis, prevention and treatment of disorders which include cell
XX proliferative disorders such as arteriosclerosis, hepatitis,
```


CC myelofibrosis, psoriasis and cancer including adenocarcinoma, leukaemia,
CC lymphoma; neurological disorders such as epilepsy, ischaemic
CC cerebrovascular disease, Alzheimer's disease, Pick's disease, dementia,
CC Parkinson's disease, ataxias, multiple sclerosis, bacterial and viral
CC meningitis, Creutzfeldt-Jakob disease, schizophrenic disorders, amnesia;
CC cardiovascular disorders such as arteriovenous fistula, atherosclerosis,
CC hypertension, vascular tumours, myocardial infarction, hypertensive heart
CC disease, infective endocarditis, cardiomyopathy, myocarditis;
CC gastrointestinal disorders such as dysphagia, peptic oesophagitis,
CC emesis, anorexia, nausea, peptic ulcer, cholelithiasis, diarrhoea,
CC constipation, acquired immune deficiency syndrome (AIDS), hepatic
CC encephalopathy; autoimmune/inflammatory disorders such as Addison's
CC disease, allergies, spondylitis, amyloidosis, anaemia, asthma, contact
CC dermatitis, Crohn's disease, diabetes mellitus, Goodpasture's syndrome,
CC emphysema, Grave's disease, gout, multiple sclerosis, rheumatoid
CC arthritis, systemic lupus erythematosus, uveitis, viral, bacterial,
CC fungal, parasitic, protozoal and helminthic infections and trauma;
CC metabolic disorders such as diabetes, obesity and osteoporosis; and viral
CC infections such as infection caused by viral agent classified as
CC adenovirus, arenavirus, bunyavirus. Polynucleotides of the invention are
CC useful as probes for assessing toxicity of test compounds. They are also
CC used in gene therapy. The present sequence is human G-protein coupled
CC receptor 3 (GCRC-3) protein
XX
SQ Sequence 346 AA;

Query Match 100.0%; Score 1853; DB 5; Length 346;
Best Local Similarity 100.0%; Pred. No. 7.4e-199;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYNGSCRIEGDTISQVMPPLIVAFVLGALNGVALCGFCFHMKTWKPSTVYLFNLVA 60
DB 1 MYNGSCRIEGDTISQVMPPLIVAFVLGALNGVALCGFCFHMKTWKPSTVYLFNLVA 60
QY 61 DELLMICLPFRDYLLRRRHAFGDI PCRVGLFTLAMNRAGSIVFLTVVAADRYKVVHP 120
DB 61 DELLMICLPFRDYLLRRRHAFGDI PCRVGLFTLAMNRAGSIVFLTVVAADRYKVVHP 120
QY 121 HNAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHIDM 180
DB 121 HNAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHIDM 180
QY 181 FOLEPMPGIILFCSFKIVSLRRQOLARQARKKATRFIMVAIVFICVLPVSAR 240
DB 181 FOLEPMPGIILFCSFKIVSLRRQOLARQARKKATRFIMVAIVFICVLPVSAR 240
QY 241 LYFLWTVPSSADPSVHGALHTLSFTYNSMLDPLVYFSPSPKFKYKLIKISLKP 300
DB 241 LYFLWTVPSSADPSVHGALHTLSFTYNSMLDPLVYFSPSPKFKYKLIKISLKP 300
QY 301 QFCHSKTORPEEMPISNLGRSCISVANSFQSDGQMDPHIVEMH 346
DB 301 QFCHSKTORPEEMPISNLGRSCISVANSFQSDGQMDPHIVEMH 346

RESULT 6
AAU11401
ID AAU11401 standard; protein; 346 AA.
XX AAU11401;
XX
XX
XX 26-FEB-2002 (first entry)
XX
XX HM74-like G-protein coupled receptor (GPCR).
XX HM74-like GPCR; G-protein coupled receptor; antibacterial; fungicide;
KW protozoacide; analgesic; cytostatic; neuroleptic; nootropic;
KW anticonvulsant; tranquilizer; viral infection; pain; cancer; anorexia;
KW bulimia; asthma; central nervous system disease; CNS disease;
KW cardiovascular disease; hypertension; hypertension; angina pectoris;
KW myocardial infarction; urinary retention; osteoporosis; ulcer; asthma;
KW inflammation; allergy; benign prostatic hypertrophy; multiple sclerosis;
KW psychotic disorder; neurological disorder; dyskinesia;

KW Huntington's disease; Tourette's syndrome; anxiety; schizophrenia;
KW manic depression; delirium; dementia; mental retardation.
XX Homo sapiens.
FH Key Location/Qualifiers
FT Domain 20..37 /label= Transmembrane_domain_1
FT Domain 53..73 /label= Transmembrane_domain_2
FT Domain 91..113 /label= Transmembrane_domain_3
FT Region 101..118 /label= GPCR region
FT Domain 133..150 /note= "G-protein coupled receptor region"
FT Domain 180..197 /label= Transmembrane_domain_4
FT Domain 223..242 /label= Transmembrane_domain_5
FT Domain 260..279 /label= Transmembrane_domain_6
FT /label= Transmembrane_domain_7
XX WO200177320-A2.
XX 18-OCT-2001.
XX 04-APR-2001; 2001WO-EP003811.
XX 05-APR-2000; 2000US-0194701P.
XX (FARB) BAYER AG.
XX Xiao Y;
XX WPI: 2002-049147/06.
XX N-PSDB; AAS18501.
XX Novel isolated polynucleotide, useful for treating infection, pain,
XX cancer, asthma, hypertension, myocardial infarction, urinary retention,
XX osteoporosis, encodes the human HM74-like G-protein coupled receptor
XX polypeptide.
XX Claim 1; Fig 2; 77pp; English.
XX The invention describes a novel isolated polynucleotide (I) encoding a
XX human HM74-like G-protein coupled receptor (GPCR) polypeptide. Reagents
XX that regulate HM74-like GPCR are useful for modulating the activity of
XX the protein in a disease selected from bacterial, fungal, protozoan, and
XX viral infection, pain, cancer, anorexia, bulimia, asthma, central nervous
XX system (CNS) disease, cardiovascular disease, hypotension, hypertension,
XX angina pectoris, myocardial infarction, urinary retention, osteoporosis,
XX ulcer, asthma, inflammation, allergy, benign prostatic hypertrophy,
XX multiple sclerosis and dyskinesia such as Huntington's disease and
XX Tourette's syndrome. The composition is also useful for treating
XX psychotic and neurological disorders such as anxiety, schizophrenia,
XX manic depression, delirium, dementia and severe mental retardation. (I)
XX or the HM74-like GPCR polypeptide are also useful for treating the above
XX mentioned diseases. (I) is useful in a diagnostic assay for detecting
XX diseases, susceptibility to diseases and abnormalities related to the
XX presence of mutations in the nucleic acid sequences which encode a GPCR.
XX The polypeptide is useful to identify test compounds which may act as
XX agonists or antagonists at the receptor site and which can be regulated
XX to provide therapeutic effects. The polypeptide is also useful as a bait
XX protein in a two-hybrid or three-hybrid assay, and to immunise a mammal
XX for production of polyclonal antibodies. This the amino acid sequence of
XX human HM74-like GPCR described in the method of the invention
XX Sequence 346 AA;
Query Match 100.0%; Score 1853; DB 5; Length 346;
Best Local Similarity 100.0%; Pred. No. 7.4e-199;

```
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYNGSCCRLEGDTISQVMPPLLIYAFVLGALNGVALCGCFHMTWKPSVTYVLENLAVA 60
Db 1 MYNGSCCRLEGDTISQVMPPLLIYAFVLGALNGVALCGCFHMTWKPSVTYVLENLAVA 60
QY 61 DFLLMICLPFRDYYLRRRHWAAGDIPCRVGLFTLAMNRAGSIVFLTVVAAADRYFKVHP 120
Db 61 DFLLMICLPFRDYYLRRRHWAAGDIPCRVGLFTLAMNRAGSIVFLTVVAAADRYFKVHP 120
QY 121 HNAVNTISTRVAAGIVCTLWALVILGTVYVLLLENHLCVQETAVSCESTIMESANGWHDIM 180
Db 121 HNAVNTISTRVAAGIVCTLWALVILGTVYVLLLENHLCVQETAVSCESTIMESANGWHDIM 180
QY 181 FOLEFFMPLGIILFCSEFKIVWSLRRRQQLARQARKKATRFIMVVAIVFITCYLPSVSAR 240
Db 181 FOLEFFMPLGIILFCSEFKIVWSLRRRQQLARQARKKATRFIMVVAIVFITCYLPSVSAR 240
QY 241 LYFLWTVPSACDPSVHGALHITLFTYVNSMLDPLVYVFFSPSPKPKYKIKSLKPK 300
Db 241 LYFLWTVPSACDPSVHGALHITLFTYVNSMLDPLVYVFFSPSPKPKYKIKSLKPK 300
QY 301 QPGHKTQRPPEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346
Db 301 QPGHKTQRPPEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346

RESULT 7
AAE17077
ID AAE17077 standard; protein; 346 AA.
AC AAE17077;
XX
XT 18-APR-2002 (first entry)
XX
DE Human G-protein coupled receptor (GPCRx14) protein.
KW Human: G-protein coupled receptor; GPCRx14; cerebroprotective; vomiting;
KW receptor-mediated disorder; therapy; urinary retention; allergy; obesity;
KW osteoporosis; angina pectoris; restenosis; atherosclerosis; hypotension;
KW anorexia; tumour; migraine; acute heart failure; ulcer; antiinflammatory;
KW stroke; hypertension; neuronal disorder; myocardial infarction psychotict;
KW depression; mental retardation; neurodegenerative disease; antibacterial;
KW Alzheimer's disease; dementia; ischaemia; Parkinson's disease; antiviral;
KW Huntington's disease; anxiety; antifungal; immunosuppressive; cytostatic;
KW vulnerary; analgesic; anorectic; anabolic; diuretic; cardiac; nootropic;
KW antiemetic; vasotropic; diabetes; cancer; tranquilizer; neuroleptic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 17..40
FT /note= "Transmembrane domain"
FT Domain 52..70
FT /note= "Transmembrane domain"
FT Domain 90..111
FT /note= "Transmembrane domain"
FT Domain 132..152
FT /note= "Transmembrane domain"
FT Domain 185..203
FT /note= "Transmembrane domain"
FT Domain 221..237
FT /note= "Transmembrane domain"
FT Domain 258..281
FT /note= "Transmembrane domain"
XX
WO200198330-A2.
XX
PD 27-DEC-2001.
XX
PF 20-JUN-2001; 2001WO-BE000104.
XX
PR 20-JUN-2000; 2000US-0212913P.
```

```
PR 11-JUL-2000; 2000US-0217494P.
PR 26-JAN-2001; 2001EP-00870015.
XX 12-FEB-2001; 2001EP-00870024.
PA (EURO-) EUROSREEN SA.
XX
PI Lannoy V, Brezillon S, Dethaux M, Parmentier M, Govarts C;
DR WPI; 2002-130789/17.
XX N-PSDB; AAD27497.
PT New G-protein coupled receptor, useful in the manufacture of medicaments
PT for treating receptor mediated disorders e.g. acute heart failure and
PT Alzheimer's disease.
XX
PS Disclosure; Page 29; 46pp; English.
XX
CC The present invention relates to a G-protein coupled receptor (GPCR) and
CC nucleotide encoding it. GPCR are useful in the manufacture of a
CC medicament for the prevention and/or treatment of receptor-mediated
CC disorders e.g. viral infections, virus and bacterial diseases, diseases or
CC and disorders involving disturbances of cell migration, diseases or
CC perturbations of immune system including cancers, development of tumours
CC and tumour metastasis, inflammatory and neoplastic processes; bacterial
CC and fungal infections, in wound and bone healing, dysfunction of
CC regulatory growth functions; pains, diabetes, obesity, anorexia, bulimia,
CC urinary retention, osteoporosis, angina pectoris, atherosclerosis,
CC restenosis, diseases involving excessive or reduced proliferation or loss
CC of smooth muscle cells, aneurysm, stroke, ischaemia, ulcers, allergies,
CC benign prostatic hypertrophy, migraine, vomiting; blood circulating
CC affections including acute heart failure, hypotension, hypertension and
CC myocardial infarction psychotict; neuronal disorders such as anxiety,
CC schizophrenia, maniac depression, depression, delirium, dementia, severe
CC mental retardation; degenerative diseases; neurodegenerative diseases
CC such as Alzheimer's disease, Parkinson's disease; and dyskinesias e.g.
CC Huntington's disease or Gilles de la Tourette's syndrome and other
CC related diseases. The present sequence is GPCRx14 protein
XX
SQ Sequence 346 AA;
Query Match 100.0%; Score 1853; DB 5; Length 346;
Best Local Similarity 100.0%; Pred. No. 7.4e-199;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYNGSCCRLEGDTISQVMPPLLIYAFVLGALNGVALCGCFHMTWKPSVTYVLENLAVA 60
Db 1 MYNGSCCRLEGDTISQVMPPLLIYAFVLGALNGVALCGCFHMTWKPSVTYVLENLAVA 60
QY 61 DFLLMICLPFRDYYLRRRHWAAGDIPCRVGLFTLAMNRAGSIVFLTVVAAADRYFKVHP 120
Db 61 DFLLMICLPFRDYYLRRRHWAAGDIPCRVGLFTLAMNRAGSIVFLTVVAAADRYFKVHP 120
QY 121 HNAVNTISTRVAAGIVCTLWALVILGTVYVLLLENHLCVQETAVSCESTIMESANGWHDIM 180
Db 121 HNAVNTISTRVAAGIVCTLWALVILGTVYVLLLENHLCVQETAVSCESTIMESANGWHDIM 180
QY 181 FOLEFFMPLGIILFCSEFKIVWSLRRRQQLARQARKKATRFIMVVAIVFITCYLPSVSAR 240
Db 181 FOLEFFMPLGIILFCSEFKIVWSLRRRQQLARQARKKATRFIMVVAIVFITCYLPSVSAR 240
QY 241 LYFLWTVPSACDPSVHGALHITLFTYVNSMLDPLVYVFFSPSPKPKYKIKSLKPK 300
Db 241 LYFLWTVPSACDPSVHGALHITLFTYVNSMLDPLVYVFFSPSPKPKYKIKSLKPK 300
QY 301 QPGHKTQRPPEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346
Db 301 QPGHKTQRPPEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346

RESULT 8
ABB08596
ID ABB08596 standard; protein; 346 AA.
XX
```

AC	ABB08596;	ID	ABG93786 standard; protein; 346 AA.
XX		XX	
DT	01-JUL-2002 (first entry)	AC	ABG93786;
XX		XX	
DE	Human lipocyte-originated G protein-coupled receptor protein TGR13.	DT	26-NOV-2002 (first entry)
XX		XX	
KW	Antiinflammatory; anorectic; obesity; inflammation; gene therapy; human;	DE	Human G protein-coupled receptor protein, nGPCR-11.
KW	G protein-coupled receptor protein TGR13.	XX	
OS	Homo sapiens.	KW	Human; receptor; G protein-coupled receptor; GPCR; nGPCR; beGPCR;
XX		KW	nG protein coupled receptor; communication; serpentine structure;
PN	WO200202767-A1.	KW	seven transmembrane receptor; 7TM; mental disorder; diagnosis;
XX		KW	genetic predisposition; brain; immune response; gene therapy;
XX		KW	anxiety disorder; depression; bipolar disorder; schizophrenia;
PD	10-JAN-2002.	KW	Huntington's disease; dyskinesia; manic depression; stroke;
XX		KW	Parkinson's disease; Alzheimer's disease; diabetes; inflammation; wound;
XX		KW	tranquilliser.
PF	02-JUL-2001; 2001WO-JP005711.	XX	
XX		OS	Homo sapiens.
PR	04-JUL-2000; 2000JP-00206860.	XX	
PR	31-JUL-2000; 2000JP-00235274.	XX	
XX		PN	WO200264789-A1.
PA	(TAKE) TAKEDA CHEM IND LTD.	XX	
XX		PD	22-AUG-2002.
PI	Shibata S, Horikoshi K, Taniyama Y, Shintani Y, Miyajima N;	XX	
XX		XX	
DR	WPI; 2002-164535/21.	PF	14-FEB-2001; 2001WO-US004641.
DR	N-PSDB; ABA99236.	XX	
XX		XX	
XX	New human lipocyte-originated G protein-coupled receptor proteins TGR13	PR	14-FEB-2001; 2001WO-US004641.
PT	and encoding DNAs, for developing drugs to treat obesity and	XX	
PT	inflammations, including gene therapy.	PA	(PHAA) PHARMACIA & UPJOHN CO.
XX		XX	
PS	Claim 1; Fig 2; 101pp; Japanese.	PI	Lind P, Parodi LA, Vogeli G, Wood LS;
XX		XX	
CC	This invention relates to a human lipocyte-originated G protein-coupled	DR	WPI; 2002-674879/72.
CC	receptor proteins TGR13, thought to be antiinflammatory and anorectic in	DR	N-PSDB; ABS70241.
CC	their action. The proteins and encoded DNAs are for use in developing	XX	
CC	drugs to treat obesity and inflammation, including gene therapy. The	PT	New nucleic acids and polypeptides of the nG protein-coupled receptor,
CC	present sequence represents the human lipocyte-originated G protein-	PT	useful for treating or diagnosing a mental disorder or a disorder
CC	coupled receptor protein TGR13	PT	affecting the brain, e.g. anxiety disorders, schizophrenia, stroke or
XX		PT	Parkinson's disease.
XX		XX	
SQ	Sequence 346' AA;	PS	Example 1; Page 84; 244pp; English.
		XX	
		CC	The invention discloses an isolated human polypeptide, and encoding
		CC	nucleic acid, for a G protein-coupled receptor (GPCR), particularly the
		CC	nG protein coupled receptor-14 (nGPCR-14). GPCRs are vital in the
		CC	communication between cells and their environment and are characterised
		CC	by a serpentine structure that passes through the cell membrane seven
		CC	times, hence the reason such receptors are sometimes called seven
		CC	transmembrane receptors (7TM). The polynucleotides and polypeptides are
		CC	useful for identifying an nGPCR allelic variant that correlates with a
		CC	mental disorder, for isolating an antibody that binds to an epitope of
		CC	the polypeptide, for identifying a compound that binds the polypeptide or
		CC	polynucleotide and/or modulates its biological activity, for screening a
		CC	human subject to diagnose a disorder, or a genetic predisposition to a
		CC	disorder, affecting the brain or a genetic disposition to the disorder,
		CC	for identifying compounds useful for the treatment of a mental disorder
		CC	and for identifying a compound useful as a modulator of binding between
		CC	nGPCR-14 and a binding partner of nGPCR-14. The polypeptide is also
		CC	useful for inducing an immune response in a mammal. The nucleic acid or
		CC	polypeptide is particularly useful, using gene therapy, for treating e.g.
		CC	anxiety disorders, depression, bipolar disorder, schizophrenia,
		CC	Huntington's disease, dyskinesias, manic depression, stroke, Parkinson's
		CC	disease or Alzheimer's disease. The nucleic acid and polypeptide may also
		CC	be used for treating diabetes, inflammation or wounds. The sequences
		CC	presented in ABG93747-ABG93793, ABG93795 and ABG93796 are the nGPCR
		CC	referred to as beGPCRs) proteins
		XX	
		SQ	Sequence 346 AA;
			Query Match 100.0%; Score 1853; DB 5; Length 346;
			Best Local Similarity 100.0%; Pred. No. 7.4e-199;
			Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MYNGSCCRIEGDTISQVMPPLLIIVAFVLGALGNVALCGFCFHMKTWKPSVYLFNLAVA 60		
Db	1 MYNGSCCRIEGDTISQVMPPLLIIVAFVLGALGNVALCGFCFHMKTWKPSVYLFNLAVA 60		
QY	61 DFLMLICLPRTDYILRRRHAFGDIPCRVGLFTLANNRAGSIVFLTVAAADRYFKVHP 120		
Db	61 DFLMLICLPRTDYILRRRHAFGDIPCRVGLFTLANNRAGSIVFLTVAAADRYFKVHP 120		
QY	121 HHAVNTISTRVAAGIYCTLMALVILGTVYLLLENHLCVQETAIVSCSFIMESANGWHDIM 180		
Db	121 HHAVNTISTRVAAGIYCTLMALVILGTVYLLLENHLCVQETAIVSCSFIMESANGWHDIM 180		
QY	181 FQLEFFMPLGIILFCSEFKIWSLRRRQQLARQARMKATRFIMVVAIVITCVLPVSAR 240		
Db	181 FQLEFFMPLGIILFCSEFKIWSLRRRQQLARQARMKATRFIMVVAIVITCVLPVSAR 240		
QY	241 LYLFWTVPSACDPSVHGALHITLSFTYNSMLDPLVYFFSSPFPKFNKLCISLKP 300		
Db	241 LYLFWTVPSACDPSVHGALHITLSFTYNSMLDPLVYFFSSPFPKFNKLCISLKP 300		
QY	301 QPGHSHKTQPEEMPISNLGRSCISVANGFSQSDGQWDPHIVEWH 346		
Db	301 QPGHSHKTQPEEMPISNLGRSCISVANGFSQSDGQWDPHIVEWH 346		
RESULT 9			
ABG93786			

Db 1 MYNGSCCRIEGDTISQVMPPLLIIVAFVLGALNGVALCGCFHMKTKPSTVYLFNLAVA 60
QY 61 DFLLMICLPFRDYLLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
Db 61 DFLLMICLPFRDYLLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
QY 121 HAVNTISTRVAAGIVCTLMALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
Db 121 HAVNTISTRVAAGIVCTLMALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
QY 181 FOLEFFMPLGIILFCSPKIVMSLRRRQQLARQARMKKATRFIMVVAIVFIITCYLPSVSAR 240
Db 181 FOLEFFMPLGIILFCSPKIVMSLRRRQQLARQARMKKATRFIMVVAIVFIITCYLPSVSAR 240
QY 241 LYFLMTVPSSACDPSVHGALHITLSFTYVNSMLDPLVYFSSPPKPFYKYLKICSLKPK 300
Db 241 LYFLMTVPSSACDPSVHGALHITLSFTYVNSMLDPLVYFSSPPKPFYKYLKICSLKPK 300
QY 301 QPGHKTQRPPEMPISNLRGRSCISVANSFQSDGQWDPHIVEWH 346
Db 301 QPGHKTQRPPEMPISNLRGRSCISVANSFQSDGQWDPHIVEWH 346

RESULT 10
ABP95599
ID ABP95599 standard; protein; 346 AA.

XX AC ABP95599;

-DT 06-MAR-2003 (first entry)

DE Human GPCR polypeptide SEQ ID NO 8.

XX KW Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
-KW drug development; gustatory; taste; fragrance; receptor.

OS Homo sapiens.

XX PN WO200216548-A2.

XX PD 28-FEB-2002.

XX PF 30-JUL-2001; 2001WO-IB001446.

XX PR 04-AUG-2000; 2000JP-00237819.

XX PR 13-FEB-2001; 2001JP-00034434.

XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX PI Haga T, Takeda S, Mitaku S;

XX DR WPI; 2002-304118/34.

XX DR N-PSDB; AB242873.

XX PT Database global search for G protein-coupled receptors, proteins and

XX PT encoded genes for studying in vivo signal transduction mechanism and

XX PT identifying targets for drug development.

XX PS Claim 10; SEQ ID NO 8; 97pp + Sequence Listing; Japanese.

XX CC The invention relates to a method for screening G protein-coupled
CC receptor (GPCR) genes (AB242870-AB243216) and/or GPCR proteins (ABP95596-
CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane
CC domains with 250-1000 amino acid residues to give a gene homologous with
CC a known GPCR gene. The receptor proteins and encoded genes are useful for
CC studying in vivo signal transduction mechanism and identifying targets
CC for drug development e.g. based on olfactory and gustatory receptors in
CC form of agonists and antagonists by screening intrinsic and extrinsic
CC ligands as bitter taste inhibitors, taste enhancers and fragrance
CC improvers. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 346 AA;
Query Match 100.0%; Score 1853; DB 5; Length 346;
Best Local Similarity 100.0%; Pred. No. 7.4e-199;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYNGSCCRIEGDTISQVMPPLLIIVAFVLGALNGVALCGCFHMKTKPSTVYLFNLAVA 60
Db 1 MYNGSCCRIEGDTISQVMPPLLIIVAFVLGALNGVALCGCFHMKTKPSTVYLFNLAVA 60
QY 61 DFLLMICLPFRDYLLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
Db 61 DFLLMICLPFRDYLLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
QY 121 HAVNTISTRVAAGIVCTLMALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
Db 121 HAVNTISTRVAAGIVCTLMALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
QY 181 FOLEFFMPLGIILFCSPKIVMSLRRRQQLARQARMKKATRFIMVVAIVFIITCYLPSVSAR 240
Db 181 FOLEFFMPLGIILFCSPKIVMSLRRRQQLARQARMKKATRFIMVVAIVFIITCYLPSVSAR 240
QY 241 LYFLMTVPSSACDPSVHGALHITLSFTYVNSMLDPLVYFSSPPKPFYKYLKICSLKPK 300
Db 241 LYFLMTVPSSACDPSVHGALHITLSFTYVNSMLDPLVYFSSPPKPFYKYLKICSLKPK 300
QY 301 QPGHKTQRPPEMPISNLRGRSCISVANSFQSDGQWDPHIVEWH 346
Db 301 QPGHKTQRPPEMPISNLRGRSCISVANSFQSDGQWDPHIVEWH 346

RESULT 11

AAO14788
ID AAO14788 standard; protein; 346 AA.

XX AC AAO14788;

XX DT 28-JUN-2002 (first entry)

XX DE Human purinergic-like G-protein coupled receptor (AXOR87).

XX KW Human; purinergic-like G-protein coupled receptor; AXOR87; immunity;
KW autoimmunity; inflammation; immunodeficiency; bacterial infection;
KW fungal infection; viral infection; protozoa infection; cancer; diabetes;
KW obesity; anorexia; bulimia; asthma; psoriasis; rheumatoid arthritis;
KW osteoarthritis; psychotic disorder; neurological disorder; vaccine;
XX chromosome 12q24.

XX OS Homo sapiens.

XX PN GB2365868-A.

XX PD 27-FEB-2002.

XX PF 25-MAY-2001; 2001GB-00012860.

XX PR 30-MAY-2000; 2000US-00580675.

XX PR 02-NOV-2000; 2000GB-00026839.

XX PA (SMK) SMITHKLINE BEECHAM CORP.

XX PA (SMK) SMITHKLINE BEECHAM PLC.

XX PI Ignar DM, Elshourbagy N, Gattu M, Shabon U;

XX DR WPI; 2002-364852/40.

XX DR N-PSDB; AAL42499.

XX PT New purinergic-like G-protein coupled receptor AXOR87 polypeptide and
XX polynucleotide, useful for treating diseases related to autoimmunity,
XX inflammation, immunodeficiency, or bacterial, fungal, viral and protozoal
XX infections.

XX Claim 2; Page 36; 47pp; English.

XX The invention comprises the amino acid and coding sequence of the human

CC purinergic-like G-protein coupled receptor AXOR87. The AXOR87 DNA and

CC protein sequences of the invention may be used for treating diseases

CC related to immunity, autoimmunity, inflammation, immunodeficiency, and

CC infections (i.e. bacterial, fungal, protozoan). The AXOR87 DNA and

CC protein sequences are particularly useful for treating: cancers,

CC diabetes, obesity, anorexia, bulimia, asthma, psoriasis, rheumatoid

CC arthritis, osteoarthritis, as well as psychotic and neurological

CC disorders. The AXOR87 DNA and protein sequences may also be used as

CC vaccines. The present amino acid sequence (encoded by a sequence located

CC on chromosome 12q24) represents the human AXOR87 protein

XX Sequence 346 AA;

Query Match 100.0%; Score 1853; DB 5; Length 346;

Best Local Similarity 100.0%; Pred. No. 7.4e-199;

Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNSCCRIEGTISQVMPPLIVAFVLGALGVNLCVQETAVSCSFIMESANGWHDIM 60

DB 1 MYNSCCRIEGTISQVMPPLIVAFVLGALGVNLCVQETAVSCSFIMESANGWHDIM 60

QY 61 DFLLMICLPFRDYDYLRRRHAFGDI PCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHP 120

DB 61 DFLLMICLPFRDYDYLRRRHAFGDI PCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHP 120

QY 121 HAVNTISPRVAGIVCTLMALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180

DB 121 HAVNTISPRVAGIVCTLMALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180

QY 181 FOLEFPMPLGIILFCSFKIWSLRRLQRLARQARKKATRFIMVAIVFITCYLPSVSAR 240

DB 181 FOLEFPMPLGIILFCSFKIWSLRRLQRLARQARKKATRFIMVAIVFITCYLPSVSAR 240

QY 241 LYFLMTVPSSACDPSVHGALHITLFTYNNMMLDPLVYFSSPKFYNNKLIKICSLRKP 300

DB 241 LYFLMTVPSSACDPSVHGALHITLFTYNNMMLDPLVYFSSPKFYNNKLIKICSLRKP 300

QY 301 QPGHKTQRPPEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346

DB 301 QPGHKTQRPPEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346

RESULT 12

AAE24354

ID AAE24354 standard; protein; 346 AA.

XX AAE24354;

XX 04-OCT-2002 (first entry)

DE Human G protein coupled receptor (GPCR), 57242 protein.

XX Human; G protein coupled receptor; GPCR; 57242 protein; overweight;

KW metabolic disorder; lipogenesis; lipolysis; immunomodulator; heart;

KW bone disorder; osteoporosis; osteogenesis; bone resorption; cachexia;

KW hyperlipidaemia; anorexia; haematopoietic disorder; osteopathic;

KW autoimmune disease; psoriasis; multiple sclerosis; brain disorder;

KW degenerative disease; Alzheimer's disease; Pick disease; diabetes;

KW adipocyte; hyperplastic growth; hypertrophic growth; gene therapy;

KW obesity; anorectic; receptor.

OS Homo sapiens.

XX

XX Key Location/Qualifiers

FT Peptide 1..37

FT Domain /label= Signal_peptide

FT 1..20

FT /note= "N-terminal non-transmembrane domain"

FT Modified-site 3..6

FT Cleavage-site /note= "N-glycosylation site"

FT 9..10

FT /note= "Cleavage site for mitochondrial preseq"

FT 21..42

FT /note= "Transmembrane domain"

FT 32..278

FT /note= "GPCR domain"

FT 38..346

FT /note= "Human mature GPCR protein"

FT 43..51

FT /note= "Non-transmembrane domain"

FT 52..70

FT /note= "Transmembrane domain"

FT 71..89

FT /note= "Extracellular loop"

FT 77..80

FT /note= "Nuclear localisation signal"

FT 90..111

FT /note= "Transmembrane domain"

FT 112..130

FT /note= "Non-transmembrane domain"

FT 131..152

FT /note= "Transmembrane domain"

FT 153..184

FT /note= "Extracellular loop"

FT 185..201

FT /note= "Transmembrane domain"

FT 202..220

FT /note= "Non-transmembrane domain"

FT 204..220

FT /note= "Nuclear localisation signal"

FT 216..219

FT /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"

FT 221..245

FT /note= "Transmembrane domain"

FT 245..258

FT /note= "Extracellular loop"

FT 246..255

FT /note= "Non-transmembrane domain"

FT 259..280

FT /note= "Transmembrane domain"

FT 281..346

FT /note= "C-terminal cytoplasmic domain"

XX WO200218579-A2.

XX 07-MAR-2002.

XX 29-AUG-2001; 2001WO-US026882.

XX 29-AUG-2000; 2000US-0228409P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Glucksmann MA;

XX WPI: 2002-479433/51.

XX N-PSDB; AAD39181.

XX Human G protein coupled receptor nucleic acid and polypeptide molecules,

PT designated 57242, useful for diagnosing, preventing or treating aberrant

PT lipogenesis or aberrant lipolysis, obesity, diabetes or bone disorders

PT (e.g. osteoporosis).

XX Claim 9; Page 112-113; 114pp; English.

XX The invention relates to G protein coupled receptor (GPCR) family member,

CC 57242 and its corresponding nucleic acid sequence. The 57242 nucleic acid

CC and polypeptide are useful for diagnosing, preventing or treating a

CC subject having or at risk of developing a metabolic disorder,

CC particularly a disorder associated with aberrant lipogenesis or aberrant

CC lipolysis, obesity or diabetes. The 57242 DNA and protein are also useful

CC for treating a subject having bone disorder, where the disorder is
 CC osteoporosis or a disorder associated with aberrant osteogenesis or
 CC aberrant bone resorption, these diseases include obesity, diabetes,
 CC hyperlipidemia, overweight, anorexia or cachexia. The 57242 DNA and
 CC protein are also useful for treating a subject having haematopoietic
 CC disorders, autoimmune disorders e.g. psoriasis and multiple sclerosis,
 CC brain disorders, degenerative diseases e.g. Alzheimer's disease and Pick
 CC disease and disorders involving heart. The 57242 nucleic acid and
 CC polypeptide are also useful for modulating adipocyte activity such as
 CC hyperplastic growth, hypertrophic growth or lipogenesis. The 57242 DNA is
 CC used in gene therapy. The present sequence is human 57242 protein
 XX
 SQ Sequence 346 AA;

Query Match 100.0%; Score 1853; DB 5; Length 346;
 Best Local Similarity 100.0%; Pred. No. 7.4e-199;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MYNGSCCRIEGDTISQVMPPLIIVAFVLGALNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
 DB 1 MYNGSCCRIEGDTISQVMPPLIIVAFVLGALNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
 QY 61 DFLLMICLPFRDYYLRRHHWAFGDI PCRVGLFTLAMNRAGSIVFLTVAADRYPKVVHP 120
 DB 61 DFLLMICLPFRDYYLRRHHWAFGDI PCRVGLFTLAMNRAGSIVFLTVAADRYPKVVHP 120
 QY 121 HAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCEFSIMESANGWHIM 180
 DB 121 HAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCEFSIMESANGWHIM 180
 QY 181 FOLEFFMPLGIILFCSEFKIWSLRRRQQLARQARKKATRTFMVAIVFITCYLPSVSAR 240
 DB 181 FOLEFFMPLGIILFCSEFKIWSLRRRQQLARQARKKATRTFMVAIVFITCYLPSVSAR 240
 QY 241 LYFLMTVPSSACDPSVHGALHITLSFTYNSMLDPLVYFSSPSPFKYKFKIICSLKPK 300
 DB 241 LYFLMTVPSSACDPSVHGALHITLSFTYNSMLDPLVYFSSPSPFKYKFKIICSLKPK 300
 QY 301 QPGHSKTORPEEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346
 DB 301 QPGHSKTORPEEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346

RESULT 13

ABP81747
 ID ABP81747 standard; protein; 346 AA.

XX AC ABP81747;

XX DT 04-MAR-2003 (first entry)

XX DE Human chemokine receptor FKSG80/GPR81 protein SEQ ID NO:668.

XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; rheumatoid arthritis; trauma;
 KW ulcer.

XX OS Homo sapiens.

XX PN WO200261087-A2.

XX PD 08-AUG-2002.

XX PF 19-DEC-2001; 2001WO-US050107.

XX

PR 19-DEC-2000; 2000US-0257144P.
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX Burmer GC, Roush CL, Brown JP;
 XX WPT; 2003-046718/04.
 XX N-PSDB; ABZ42592.
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 PT autoimmune diseases.

XX Disclosure; Fig 1; 523pp; English.

PS The present invention describes antigenic peptides (I) comprising: (a)
 XX any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular G
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity or
 CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 CC antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention

XX Sequence 346 AA;

Query Match 100.0%; Score 1853; DB 6; Length 346;
 Best Local Similarity 100.0%; Pred. No. 7.4e-199;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNGSCCRIEGDTISQVMPPLIIVAFVLGALNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
 DB 1 MYNGSCCRIEGDTISQVMPPLIIVAFVLGALNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
 QY 61 DFLLMICLPFRDYYLRRHHWAFGDI PCRVGLFTLAMNRAGSIVFLTVAADRYPKVVHP 120
 DB 61 DFLLMICLPFRDYYLRRHHWAFGDI PCRVGLFTLAMNRAGSIVFLTVAADRYPKVVHP 120
 QY 121 HAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCEFSIMESANGWHIM 180
 DB 121 HAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCEFSIMESANGWHIM 180
 QY 181 FOLEFFMPLGIILFCSEFKIWSLRRRQQLARQARKKATRTFMVAIVFITCYLPSVSAR 240
 DB 181 FOLEFFMPLGIILFCSEFKIWSLRRRQQLARQARKKATRTFMVAIVFITCYLPSVSAR 240
 QY 241 LYFLMTVPSSACDPSVHGALHITLSFTYNSMLDPLVYFSSPSPFKYKFKIICSLKPK 300
 DB 241 LYFLMTVPSSACDPSVHGALHITLSFTYNSMLDPLVYFSSPSPFKYKFKIICSLKPK 300
 QY 301 QPGHSKTORPEEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346
 DB 301 QPGHSKTORPEEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346

Db	61	DELLMICLPFRDYLRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVAADRYFKVHP	120
Qy	121	HHAVNTISTRVAGIVCTLMALVILGTVYLLLENHLCVOETAVSCSFIMESANGWHDIM	180
Db	121	HHAVNTISTRVAGIVCTLMALVILGTVYLLLENHLCVOETAVSCSFIMESANGWHDIM	180
Qy	181	FOLEFFMPLGIILFCSFKIWSLRROQLARQARMKKATRFIMVVAIVFITCYLPSVSAR	240
Db	181	FOLEFFMPLGIILFCSFKIWSLRROQLARQARMKKATRFIMVVAIVFITCYLPSVSAR	240
Qy	241	LYFLWTVPSACDPSVHGALHITLFTYMNMSMLDPLVYVSSPSPKFYNKIKICSLKPK	300
Db	241	LYFLWTVPSACDPSVHGALHITLFTYMNMSMLDPLVYVSSPSPKFYNKIKICSLKPK	300
Qy	301	QFGHKTQRPPEMPIISNLGRRSCISVANSFQSQSDGQMDPHIVEWH	346
Db	301	QFGHKTQRPPEMPIISNLGRRSCISVANSFQSQSDGQMDPHIVEWH	346

Search completed: August 30, 2005, 18:30:49
Job time : 169 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2005, 18:24:37 ; Search time 41 Seconds
(without alignments)
811.976 Million cell updates/sec

Title: US-10-719-692-6
Perfect score: 1853
Sequence: 1 MINGSCCRIEGDTISQVMP.....ANSFQSQDQWDPHIVEWH 346

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	880.5	47.5	387	2 I69202	G protein-coupled
2	364	19.6	362	2 S33733	G protein-coupled
3	362.5	19.6	373	2 JC4162	P2Y receptor - bov
4	354	19.1	373	2 JC4737	G protein-coupled
5	343.5	18.5	370	2 JC5549	heptahelical p2ys-
6	339	18.3	308	2 I50241	G protein-coupled
7	324	17.5	344	2 T09508	intron 17 purinerg
8	320	17.3	373	2 A47556	ATP receptor P2u -
9	310.5	16.8	420	2 I51667	thrombin receptor
10	309.5	16.7	363	2 I57940	somatostatin recep
11	307	16.6	391	2 C41795	somatostatin recep
12	305.5	16.5	391	2 A41795	somatostatin recep
13	305.5	16.5	391	2 A3297	somatostatin recep
14	304.5	16.4	359	2 S15403	angiotensin II rec
15	302.5	16.3	369	2 B41795	somatostatin recep
16	302	16.3	364	2 JQ1488	bradykinin B2 rece
17	302	16.3	399	2 I48705	proteinase activat
18	300.5	16.2	369	2 D41795	somatostatin recep
19	300.5	16.2	369	2 A45291	somatostatin recep
20	300	16.2	328	2 I55450	G protein-coupled
21	300	16.2	384	2 A47249	brain-specific som
22	300	16.2	428	2 A44021	somatostatin recep
23	299.5	16.2	369	2 JC2083	somatostatin recep
24	299	16.1	388	2 JN0605	somatostatin recep
25	298.5	16.1	418	2 A46226	somatostatin recep
26	298.5	16.1	432	2 A43448	thrombin receptor
27	298	16.1	428	2 S30508	probable G protein
28	297	16.0	397	2 S66518	proteinase-activat
29	296.5	16.0	346	2 S29248	somatostatin recep

angiotensin II rec
P-2U nucleotide re
somatostatin recep
delta opioid recep
G protein-coupled
G protein-coupled
angiotensin II rec
angiotensin II rec
angiotensin II rec
delta opioid recep
angiotensin II rec
chemokine (C-C) re
delta opioid recep
G protein-coupled
probable chemotr
angiotensin II rec
allatostatin recep

30 296 16.0 359 2 A48857
31 296 16.0 375 2 A54946
32 295 15.9 384 2 JC4629
33 294 15.9 372 2 I38532
34 292.5 15.8 361 2 JC5653
35 292 15.8 371 2 JC5498
36 291.5 15.7 359 2 S44425
37 291.5 15.7 359 2 JC2134
38 290 15.7 372 2 S34592
39 289 15.6 359 2 JC1104
40 288 15.5 355 2 A45177
41 288 15.5 372 2 B48227
42 287.5 15.5 365 2 S68208
43 287.5 15.5 371 2 JC5796
44 286.5 15.5 359 2 JH0621
45 286.5 15.5 423 2 JC7677

ALIGNMENTS

RESULT 1

I69202
G protein-coupled receptor HM74 - human
C:Species: Homo sapiens (man)
C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C:Accession: I69202
R:Nomura, H.; Nielsen, B.W.; Matsushima, K.
Int. Immunol. 5, 1239-1249, 1993
A>Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chemokine receptor
A:Reference number: 154751; MUID:94092629; PMID:7505609
A:Accession: I69202
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-387 <RES>
A:Cross-references: UNIPROT:P49019; GB:D10923; NID:g219866; PIDN:BAA01721.1; PID:g219867
C:Genetics:
A:Gene: HM74
C:Superfamily: G protein-coupled receptor 4

Query Match 47.5%; Score 880.5; DB 2; Length 387;
Best Local Similarity 52.2%; Pred. No. 3.2e-73;
Matches 178; Conservative 49; Mismatches 107; Indels 7; Gaps 4;

QY 5 SCCRIEGDTISQVMPPLIIVAFVLGALGNGVALCGFCPHMKTKPSTVYLFNLAVADFL 64
Db 17 NCCVFRDDFIARVLPVPLGLGFIFGLLNGLALWIFCFHLKSWKSRIFLNLAVADFL 76
QY 65 MICLPFRDTYYLRRRHMAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYKVVHPHHA 124
Db 77 IICLPFVMDYVRRSDMNFQDIPCLRLVLFMFAMNRQSGIIFLTVAVDYPRVHPHHA 136
QY 125 NTISTRVAGIVCTLWALVILGTVYLLNHLHCVQETAVSCSFESFMSANGHHDIMFQLE 184
Db 137 KNISNWTAAIISCLLWITVGLTVHLLKKLLIQNGPANVCISFSICHTFRWHEAMFLE 196
QY 195 FPMPLGIITLFCSPKTVWSLRRQOLARQARKKATFTFMVAIVFITCVLPSSVRLVFL 244
Db 197 FLPLGIITLFCSARLIWSLRQR-QMDRAKTKRAITFTFMVAIVFVICFLPSSVVRIRIF 255
QY 245 WTVPSA--CD--PSVHGALHITLSFTYMSMLDPLVYFSSPSFPFKYKCLKICSLKP 299
Db 256 WLLHTSGTQNEVRSVDLAFITLSFTYMSMLDPLVYFSSPSFPFPFSTLINRCLQR 315
QY 300 KQPGHSKTRPEEMPISNLGRRCISIVANSFQSQDQWD 340
Db 316 KWTGPDNNRSTSVELTGDPNKT-RGAPEALMANGSEPWP 355

RESULT 2

S33733
G protein-coupled receptor - chicken
C:Species: Gallus gallus (chicken)

CjDate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
CjAccession: S33733
R;Webb, T.E.; Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burnstock
FBBS Lett. 324, 219-225, 1993
A>Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.
A;Reference number: S33733; MUID:93285340; PMID:8508924
A;Accession: S33733
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-362 <WEB>
A;Cross-references: UNIPROT:P34996; EMBL:X73268; NID:G395084; PIDN:CAA51716.1; PID:G3950
A;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 19.6%; Score 364; DB 2; Length 362;
Best Local Similarity 29.1%; Pred. No. 9.5e-26;
Matches 95; Conservative 58; Mismatches 130; Indels 44; Gaps 7;

QY 18 MPPLLIIVAFVLGALNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRDYYLR 77
Db 43 LPTVILVPIITGFLGNSVAIWMFVHMRPWSGISVYMFNLALADFLYVLTLPALIFYFVN 102
QY 78 RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHPHNAVNTISTRVAAGIVC 137
Db 103 KTDWIFGDVCKLQRFIFHVNLYSGILFLTCISVHRVTGVVHPLKSLGRLKKGNVYVSS 162
QY 138 TLWALVIL-----GTVYLLENHLCVQSTA-----VSCSFINESANGWHD 178
Db 163 LVMLVAVIAPIPLFYSGTGVRRNKTITCYDTTADYLRSYFYVSMCTTVFM----- 214
QY 179 IMFQLEFFMGLGIILFCSPKIVMSLRRRQOLARQARKKATRFIMVAIVFITCYLP--- 235
Db 215 -----FCIPPIVILCCYGLIVKALYIK-DLDNSPLRRKSIYLIIVLTVFAVSILPHV 267
QY 236 ----SVSARLYFLWTPVSSACDPSVHGALHITLSFTYVNSMLDPLVYFSSPFPKFNK 291
Db 268 MKTLNLRALDF-QTPQCAFNDKVVATYQVTRGLASLNSCVDPILYFLAGDTFRRLLSR 326
QY 292 LKICSLKPKQGHKTQRPPEEMPISNL 318
Db 327 ATRKSSRRSEP--NVQSKSEENTNLIL 351

RESULT 3
JC4162
P2Y receptor - bovine
C;Species: Bos primigenius taurus (cattle)
CjDate: 12-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
CjAccession: JC4162
R;Henderson, D.J.; Elliot, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.
Biochem. Biophys. Res. Commun. 212, 648-656, 1995
A>Title: Cloning and characterisation of a bovine P2Y receptor.
A;Reference number: JC4162; MUID:95352058; PMID:7626079
A;Accession: JC4162
A;Molecule type: mRNA
A;Residues: 1-373 <HEN>
A;Cross-references: UNIPROT:P48042; EMBL:X87628; NID:g1032484; PIDN:CAA60958.1; PID:g103
A;Experimental source: aortic endothelial cell
C;Genetics:
A;Gene: bopv2Y
C;Superfamily: ATP receptor P2u
C;Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
F;52-77/Domain: transmembrane #status predicted <TM1>
F;88-111/Domain: transmembrane #status predicted <TM2>
F;124-150/Domain: transmembrane #status predicted <TM3>
F;171-191/Domain: transmembrane #status predicted <TM4>
F;214-237/Domain: transmembrane #status predicted <TM5>
F;261-282/Domain: transmembrane #status predicted <TM6>
F;305-328/Domain: transmembrane #status predicted <TM7>
F;11,27,113,197/Binding site: carbonylrate (Asn) (covalent) #status predicted
F;258/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 19.6%; Score 362.5; DB 2; Length 373;

Best Local Similarity 27.5%; Pred. No. 1.3e-25;
Matches 92; Conservative 68; Mismatches 140; Indels 35; Gaps 7;

QY 18 MPPLLIIVAFVLGALNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRDYYLR 77
Db 54 LPAYIILVFIITGFLGNSVAIWMFVHMRPWSGISVYMFNLALADFLYVLTLPALIFYFVN 113
QY 78 RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHPHNAVNTISTRVAAGIVC 137
Db 114 KTDWIFGDVCKLQRFIFHVNLYSGILFLTCISAHRSVGVVYPLKSLGRLKKGNVYISV 173
QY 138 TLWALVILGTVYLLLENHLCVQET-AVSC-----ESFIMESANGWHDIMFOLEPFM 187
Db 174 LVMLIVVVGISPIILFYSGTGIKRNKTITCYDTTDEYLRSYFIYSM-----CTTVAMFCV 228
QY 188 PLGIILFCSPKIVMSLRRRQOLARQARKKATRFIMVAIVFITCYLP-----SVSAR 240
Db 229 FLVILGTCYGLIVKALYIK-DLDNSPLRRKSIYLIIVLTVFAVSIFPFHVMKTNLRAR 287
QY 241 LYFLWTPVSSACDPSVHGALHITLSFTYVNSMLDPLVYFSSPFPKFNKIKICSLKPK 300
Db 288 LDF-QTEMCAFNDKVVATYQVTRGLASLNSCVDPILYFLAGDTFRRLLSR----- 337
QY 301 QPGHKTQRPPEEMPISNLRRSCISVANSFQSQSD 335
Db 338 -ATTRKASRRSEANLQSKSEDMTNLILSEFPKQNGD 370

RESULT 4
JC4737
G protein-coupled receptor P2Y1 - human
N;Alternate names: P2Y1 purinergic receptor; P2Y1 purinoceptor
C;Species: Homo sapiens (man)
CjDate: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
CjAccession: JC4737; JC4615; S54253
R;Janssens, R.; Communi, D.; Piroton, S.; Samson, M.; Parmentier, M.; Boeynaems, J.M.
Biochem. Biophys. Res. Commun. 221, 588-593, 1996
A>Title: Cloning and tissue distribution of the human P2Y1 receptor.
A;Reference number: JC4737; MUID:96205320; PMID:8630005
A;Accession: JC4737
A;Molecule type: DNA
A;Residues: 1-373 <JAN>
A;Cross-references: UNIPROT:P47900; GB:S81950; NID:g1839438; PIDN:AAB47091.1; PID:g18394
R;Ayyanathan, K.; Webb, T.E.; Sandhu, A.K.; Athwal, R.S.; Barnard, E.A.; Kunapuli, S.P.
Biochem. Biophys. Res. Commun. 218, 783-788, 1996
A>Title: Cloning and chromosomal localization of the human P2Y1 purinoceptor.
A;Reference number: JC4615; MUID:96158962; PMID:8579591
A;Accession: JC4615
A;Molecule type: mRNA
A;Residues: 1-373 <AYY>
A;Cross-references: GB:U42029; NID:g1147730; PIDN:AAA97872.1; PID:g1147731
A;Experimental source: erythro leukemia cells
R;Leon, C.; Vial, C.; Cazenave, J.; Gachet, C.
submitted to the EMBL Data Library, May 1995
A;Description: Cloning of a human putative P2Y receptor.
A;Reference number: S54253
A;Accession: S54253
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-137,139-373 <LEO>
A;Cross-references: EMBL:249205; NID:g798835; PIDN:CAA89066.1; PID:g798836
C;Comment: This receptor belongs to a family of G protein-coupled receptors. It responds
C;Genetics:
A;Gene: p2Y1; GDB:P2RY1
A;Cross-references: GDB:677125; OMIM:601167
A;Map position: 3pter-3qter
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
F;52-77/Domain: transmembrane #status predicted <TM1>
F;88-111/Domain: transmembrane #status predicted <TM2>
F;124-152/Domain: transmembrane #status predicted <TM3>
F;171-191/Domain: transmembrane #status predicted <TM4>
F;214-237/Domain: transmembrane #status predicted <TM5>

intron 17 purinergic receptor P2Y5 - human
N:Alternate names: G-protein coupled receptor
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T09508
R:Bohm, S.K.; Trump, A.; Khtin, L.M.; Kong, W.; Payan, D.G.; Bunnett, N.W.
A:Description: The human purinergic receptor P2Y5 is encoded in intron 17 of the retinoblastoma gene.
A:Reference number: Z16705
A:Accession: T09508
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-344 <BOH>
A:CROSS-references: UNIPROT:P43657; EMBL:AF000546; NID:g2232068; PID:g2232069
C:Genetics:
C:Superfamily: ATP receptor P2u
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 17.5%; Score 324; DB 2; Length 344;
Best Local Similarity 30.1%; Pred. No. 4.3e-22;
Matches 88; Conservative 56; Mismatches 120; Indels 22; Gaps 10;

QY 24 VAFVLGALNGVALCGFCFHMKTWKPSTVYLFNLAADFLMCLPFRDYLRRHWAF 83
DB 26 MVFVLGVSNCVAIFIVCLVKRNETTYMINLMSDLLFVTLPRIL-FYFTRNWP 84

QY 84 GDIPCRVGLFTLAMNRAGSIVFLTVVAADRYKVVHPHNAVNTISTRVAAGIVCT-LWAL 142
DB 85 GDLCKISVMLFVTNMYGSIPLTCTISVDRLAIVVPPKS-KTLRTKNAKIVCTGVMLT 143

QY 143 VILGT--VYLLLENHLCVQETAVSCSFIMESANGWHIMFQI-----EFFMGLIIL 193
DB 144 VIGGSAPAVFVOSTHQQGNNAEACFENPEAT--WKTYLSRIVFIEIVGFFPLILNV 201

QY 194 FCSFKIVWSLRQQLARQARK-KATRFIMVAIVFITYCLP-SVSAARLYFL---WTVP 248
DB 202 TCSSMVLKLTQKPVLSRSKINKTKVLMIFVHLIIFCFVYPVYNILNLSLVRTQTFV 261

QY 249 SSACDPSVHGALHITLSFTYMNMLDPLVYFSSPFPKFKYKIKI 294
DB 262 NCSVVAARTWYPTILCIAVSNCCDPVYYFTSDT---IQNSIKM 304

RESULT 8
ATP receptor P2u - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: A47556
R:Juscig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993
A:Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells.
A:Reference number: A47556; MUID:93281707; PMID:7685114
A:Accession: A47556
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-373 <IUS>
A:CROSS-references: UNIPROT:P35383; GB:I14751; NID:g309457; PID:AAA39871.1; PID:g309458
C:Superfamily: ATP receptor P2u
C:Keywords: transmembrane protein

Query Match 17.3%; Score 320; DB 2; Length 373;
Best Local Similarity 30.1%; Pred. No. 1.1e-21;
Matches 98; Conservative 44; Mismatches 150; Indels 34; Gaps 8;

QY 4 GSCCRIEGTISQVMPPLIIVAFVLGALNGVALCGFCFHMKTWKPSTVYLFNLAADFL 63
DB 22 GYKCRNEDFKVILPVSVGVVCLNVALYIFLCRLKTNASTIMPHLAVDSL 81

QY 64 LMICLPFRDYLLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYKVVHPHHA 123
DB 82 YAAASLPLLVYVARGDHPFSTVLCKLVRFVTLNLYCSILFELTCTISVHRCGLGLRPLHS 141

QY 124 VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCSF-----TIMESAN 174
DB 142 LRWGARYARVAAVVWVYLACQAPVLYFVTTSVRGTRITCHDTSARELSHFVAYSS- 200

QY 175 GWHIDIMFOLEFPMPLGIILFCSFKIVMSLRRRQ-----LARQARKKATRFIMVVA 226
DB 201 ----VMLGLLFAVPFVSILVC--YVLMARLLKPAYVTTGGLPRAKR--KSVRTIALVL 251

QY 227 IVFITCYLP-SVSAARLYFLMTVPSSACDP--SVHGALHITLSFTYMNMLDPLVYFSSP 283
DB 252 AVFALCFPLFHVTRTYLSFRSLDISCHTLNAINNAVKITRPLASANGCLDPLVYFLAQ 311

QY 284 SFPFKYKIKICSCLKPKQPGHKTQR 309
DB 312 RLVRPARDAK----PPTETPSPQAR 333

RESULT 9
151667
thrombin receptor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I51667
R:Gerzsten, R.E.; Chen, J.; Ishii, M.; Ishii, K.; Nanevich, T.; Turck, C.W.; Vu, T.H.;
Nature 368, 648-651, 1994
A:Title: Thrombin receptor's specificity for agonist peptide is determined by its extracellular domain.
A:Reference number: I51667; MUID:94195429; PMID:8145852
A:Accession: I51667
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-420 <GER>
A:CROSS-references: UNIPROT:P47749; EMBL:U09632; NID:g495197; PID:AAA18498.1; PID:g495198

Query Match 16.8%; Score 310.5; DB 2; Length 420;
Best Local Similarity 28.0%; Pred. No. 9.3e-21;
Matches 88; Conservative 56; Mismatches 133; Indels 37; Gaps 10;

QY 14 ISQWPPILLIIVAFVLGALNGVALCGFCFHMKTWKPSTVYLFNLAADFLMCLPFRD 73
DB 100 LTKFVPSLYTVFIVGLPLNLLAIIFLKMVKRPVAVVYMLNLAIAADVFFVSLPFKIA 159

QY 74 YLRRRHWAAGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYKVVHPHNAVNTISTRVAA 133
DB 160 YHLSGNDMLFGPGRIVTALFYCNMYSVLLIASIVDRFLAVVYPMHLSW-RTMGR 218

QY 134 GIVCT-LWALVILGTVYLL--ENHLCVQETAVSCSFIMESANGWHIMFQI-----LEF 185
DB 219 YMCSFIWLISIASTIPLLVTEQTKIPRLDITTDVLDLKLKDFIYIYFSSFCLLFF 278

QY 186 FMPGLIILFCFKIVMSLRRRQQLARQARKKATRFIMVAIVFITC-----YL 234
DB 279 FVPFIITTCYIGIRSL-SSSSIENSCCKTRALFLAVVLCVFTICFGPTNVLFTHYL 337

QY 235 PSVSAARLYFLMTVPSSACDPVHGALHITLSFTYMNMLDPLVYFSSPFPKFKYKIKI 294
DB 338 QEANEFLYFAYIL--SACVGSV-----SCCLDPLIYIYASSQQRYLSL-L 381

QY 295 CSLKPKQPGHKTQ 308
DB 382 CCRKVSEFGSSTGQ 395

RESULT 10
157940
somatostatin receptor 5 - rat
N:Alternate names: somatostatin release-inhibiting factor subtype 28 receptor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: I57940; I57949; S39244
R:O'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.
Mol. Pharmacol. 42, 939-946, 1992
A:Title: Molecular cloning and expression of a pituitary somatostatin receptor with pref

A;Reference number: I57940; MUID:93125499; PMID:1362243
A;Accession: I57940
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-363 <OCA1>
A;Cross-references: UNIPROT:P30938; GB:I04535; NID:g409238; PIDN:AAAI7029.1; PID:g409238
R;O'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.
Mol. Pharmacol. 44, 1278, 1993
A;Title: Molecular cloning and expression of a pituitary somatostatin receptor with pref
A;Reference number: I57949; MUID:94088493; PMID:8264565
A;Accession: I57949
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 341-363 <OCA2>
A;Cross-references: GB:S67370; NID:g455947; PIDN:AAB29371.1; PID:g455948
A;Experimental source: pituitary
R;Penetta, R.; Greenwood, M.; Patel, Y.C.
submitted to the EMBL Data Library, August 1993
A;Description: Correction of the nucleotide and amino acid sequence of the rat somatost
A;Reference number: S39244
A;Accession: S39244
A;Molecule type: mRNA
A;Residues: 309-363 <PEN>
A;Cross-references: EMBL:X74828; NID:g433911; PIDN:CRA52825.1; PID:g433912
C;Genetics:
A;Gene: SSTR5
C;Superfamily: vertebrate rhodopsin

Query Match 16.7%; Score 309.5; DB 2; Length 363;
Best Local Similarity 29.6%; Pred. No. 9.8e-21;
Matches 96; Conservative 53; Mismatches 148; Indels 27; Gaps 9;

QY 17 VMPPLLIIVAVLGLGALGVALCGFCFHMKTWKPSTVYLFNLAVADFLMCLICLPFRDYYL 76
Db 39 LVPVLVLLVCTVGLSNTLIVYVLRHAKMTVTNVIILNLAVADFLMGLPFLATQNA 98

QY 77 RRRHWAFGDIPCRVGLFTLAMRAGSIVFLTVVAADRYFKVHPHVAANTISTRVAAGIV 136
Db 99 VVSYPFGSFLCLVMTLDGINTQFTSIFCLWMSVDRLAVVHPPLRSARWRPRVAKMAS 158

QY 137 CTLWALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIMFO----LSEFFMPLGII 192
Db 159 AAVWVESLMSLPLLV--PADVQEGWGTCTNLSNPEPVGLWGAFAITYTSLVGLFGPLVI 216

QY 193 LFCSFIVWSLR---RQQLARQARK-KATRIMVVAIVFICVLPSSVARSILYFL-WTV 247
Db 217 CLCYLLIVVKVKAAGMRVSSRRRRSEPKVTRMVVVVLFVFGCWLFPFFIVINVLAFTL 276

QY 248 PSSACDPSVHGALHITLSFTYMNMLDPLVYFSSPSPFKFYNKLKIC-----SLKP 299
Db 277 PE---EPTSGAGLYFFVVVLSYANSCANPLYGLFSDNFRQSPFKV-LCLRRGVGMEDADA 332

QY 300 KQFGHSKTORPEMPISNLGRRC 323
Db 333 IEPRPDKGRQP---ATLPTRSC 352

RESULT 11
C41795
somatostatin receptor 1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: C41795
R;Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A;Title: Cloning and functional characterization of a family of human and mouse somatost
A;Reference number: A41795; MUID:92108031; PMID:1346068
A;Accession: C41795
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-391 <YAM>
A;Cross-references: UNIPROT:P30873; GB:M81831; NID:g201058; PIDN:AAAS8255.1; PID:g201058
C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein

Query Match 16.6%; Score 307; DB 2; Length 391;
Best Local Similarity 25.7%; Pred. No. 1.8e-20;
Matches 85; Conservative 62; Mismatches 130; Indels 54; Gaps 9;

QY 4 GSCCRIBGD-----TISQVMPPLLIIVAFV-----LQALNGVALCGF 40
Db 24 GACSRGPGSGAAGMEEPFNASQNTLSEGQSAILISFIYSVVCVLGLCGNSMVIYI 83

QY 41 CPHMKTWKPSTVYLFNLAVADFLMCLICLPFRDYYLRRRHWAFGDIPCRVGLFTLAMNRA 100
Db 84 LRYAKMTATNIYIILNLAIADDELLMSVFLVTSYL-LRHWPFGALLCLRLVLSVDAVWF 142

QY 101 GSIVELTVVAADRYFKVHPHVAANTISTRVAAGIVCTLMALVILGTVYLLLENHLCV-Q 159
Db 143 TSIYCLTVLSVDVRYVAVVHPHPIKAAARYRPTVAKVNVGLVWVLSLLVILPIVVFSTRSAA 202

QY 160 ETAVSCSFIMESANGWHD----IMFQLEFFMPLGIIILFC-----SFKIIVWSLR 204
Db 203 DGTVACNMLMPEPAQRWLGVFLYTLFMGFLIPVGAICLCYVLIITAKRMVVALKAGWQOR 262

QY 205 RQQLARQARKKATRIMVVAIVFICVLPSSVARSILYFLTVPSACDPSVHGALHITL 264
Db 263 KRSE-----RKITLMVMVMVVFICWMPFYVQVLNVVFAEQDDAT-----VSQLSV 309

QY 265 SPTYMNMLDPLVYFSSPSPFKFYNKLKIC 295
Db 310 ILGYANSCANPLYGLFSDNFRQSPFORI-LC 339

RESULT 12
A41795
somatostatin receptor 1 - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A41795
R;Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A;Title: Cloning and functional characterization of a family of human and mouse somatost
A;Reference number: A41795; MUID:92108031; PMID:1346068
A;Accession: A41795
A;Molecule type: DNA
A;Residues: 1-391 <YAM>
A;Cross-references: UNIPROT:P30872; GB:M81829; NID:g307433; PIDN:AAAS8247.1; PID:g307434
A;Note: sequence extracted from NCBI backbone (NCBIN:74767, NCBIP:74768)
C;Genetics:
A;Gene: GDB:SSTR1
A;Cross-references: GDB:I34185; OMIM:182451
A;Map position: 14q13-14q13
A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; ph
F;58-84/Domain: transmembrane #status predicted <TM1>
F;95-120/Domain: transmembrane #status predicted <TM2>
F;132-153/Domain: transmembrane #status predicted <TM3>
F;173-195/Domain: transmembrane #status predicted <TM4>
F;220-250/Domain: transmembrane #status predicted <TM5>
F;269-296/Domain: transmembrane #status predicted <TM6>
F;302-326/Domain: transmembrane #status predicted <TM7>
F;4-44, 48, 381/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;130-208/Disulfide bonds: #status predicted
F;172/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predi
F;265/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predi
F;339/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 16.5%; Score 305.5; DB 2; Length 391;
Best Local Similarity 26.3%; Pred. No. 2.5e-20;
Matches 81; Conservative 62; Mismatches 128; Indels 37; Gaps 8;

QY 10 EGDITISQVMPPLLIIVAFV-----LQALNGVALCGFCFHMKTWKPSTVYLFNLAVADFL 63
Db 47 QNGTLSEGQSAILISFIYSVVCVLGLCGNSMVIYILRYAKMTATNIYIILNLAIADSL 106

```

QY 64 LMICLPFRDYLLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVPHPHA 123
Db 107 LMLSVPFLVSTL-LRHWPFGALLCRVLVSVDVAVNMFTSIYCLTVLSVDVRYVAVVHPPIKA 165
QY 124 VNTISTRVAAGIVCTLMALVILGTVYLLLENHLCV-QETAVSCSFIMESANGMHD---- 178
Db 166 ARYRRPTAKVNLGVWVLSLLVILPIVVFSTRTAANSDDGTACVACNMLMPEPAQRWLGVFL 225
QY 179 IMFQLEFFMPLGIILFC-----SFKIIVSLRRRQQLARQARMKKATRFIMVVAI 227
Db 226 YTFLMGFLLPVGAICLCYVLLIIAKMRMVALKAGWQQRKSE-----RKITLWMVMVM 278
QY 228 VFITCPLPSVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNMSMLDPLVYFSSPSPPK 287
Db 279 VFVICWMPFYVQLVNVFAEQDDAT-----VSQLSVILGYANSKANPILYGLSDNFKR 332
QY 288 FYNKLKIC 295
Db 333 SFQRI-LC 339

RESULT 13
A39297
somatostatin receptor - rat
N:Alternate names: probable G-protein-coupled receptor; SRIF receptor
C:Species: Rattus norvegicus (Norway rat)
C>Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 09-Jul-2004
C:Accession: A39297; A45102; S20088
R:Meyerhof, W.; Paust, H.J.; Schoenrock, C.; Richter, D.
DNA Cell Biol. 10, 689-694, 1991
A:Title: Cloning of a cDNA encoding a novel putative G-protein-coupled receptor expressed
A:Reference number: A39297; MUID:92096119; PMID:1661599
A:Accession: A39297
A:Molecule type: mRNA
A:Residues: 1-391 <MEY>
A:Cross-references: UNIPROT:P28646; GB:X62314; GB:X61630; NID:g56309; PIDN:CAA44193.1; E
A:Experimental source: brain
A>Note: It is uncertain whether Met-1 is the initiator or whether translation is initiated
R:Bi, X.G.; Forte, M.; North, R.A.; Ross, C.A.; Snyder, S.H.
J. Biol. Chem. 267, 21307-21312, 1992
A:Title: Cloning and expression of a rat somatostatin receptor enriched in brain.
A:Reference number: A45102; MUID:93016064; PMID:1400442
A:Accession: A45102
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-391 <LI>
A:Experimental source: brain
A>Note: sequence extracted from NCBI backbone (NCBIP:116692)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein

Query Match 16.5%; Score 305.5; DB 2; Length 391;
Best Local Similarity 26.3%; Pred. No. 2.5e-20;
Matches 81; Conservative 62; Mismatches 128; Indels 37; Gaps 8;

QY 10 EGDTSQVNPPLLIIVAFV-----LQALNGVALCGFCFHMKTWPKSTVYLFNLAVADPL 63
Db 47 QNGTLSEGGQGSALISFIYSVCLVGLCGNSMVIYILRYAKMTATNIYILNLAIDEL 106
QY 64 LMICLPFRDYLLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVPHPHA 123
Db 107 LMLSVPFLVSTL-LRHWPFGALLCRVLVSVDVAVNMFTSIYCLTVLSVDVRYVAVVHPPIKA 165
QY 124 VNTISTRVAAGIVCTLMALVILGTVYLLLENHLCV-QETAVSCSFIMESANGMHD---- 178
Db 166 ARYRRPTAKVNLGVWVLSLLVILPIVVFSTRTAANSDDGTACVACNMLMPEPAQRWLGVFL 225
QY 179 IMFQLEFFMPLGIILFC-----SFKIIVSLRRRQQLARQARMKKATRFIMVVAI 227
Db 226 YTFLMGFLLPVGAICLCYVLLIIAKMRMVALKAGWQQRKSE-----RKITLWMVMVM 278
QY 228 VFITCPLPSVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNMSMLDPLVYFSSPSPPK 287

Query Match 16.4%; Score 304.5; DB 2; Length 359;
Best Local Similarity 24.9%; Pred. No. 2.8e-20;
Matches 81; Conservative 68; Mismatches 143; Indels 33; Gaps 8;

QY 17 VMPELLIVAFVLGALNGVALCGFCFHMKTWPKSTVYLFNLAVADPLLMICLPFRDYLL 76
Db 30 MIPTLYSIIFVVGIFGSLVIVIVFYMKLTVASVFLNLALADLCFLLTPLWAVTA 89
QY 77 RRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVPHPHVAINTISTRVAAGIV 136
Db 90 MEYRWPFNGVILCKIASASVSFNLYASVPLLCISIDRYLAIVHPMKS-RLRRTMLVAKVT 148
QY 137 C-TLWALVILGTVYLL-ENHLCVQETAVSCSFIMESANGMHDIMFOLE----FFMPL 189
Db 149 CIIWLLAGLASLPTIHRNVFFIENITITVCAPHYESQNSTLPVGLGLTKNLLGLFLPFF 208
QY 190 GIILFCSPKIVMSLRRRQQLARQARMKKATRFIMVVAIV--FITCYLP----SVSARLYF 243
Db 209 -LIILTSYLLWTKLKAYEIQKNPKRDKDIFKIILAIVLFFFSWVPHQITTFMDVLIQ 267
QY 244 LWTVPSSACDPSVHGALHITLSFTYMNMSMLDPLVYFSSPSPPKPY----- 289
Db 268 LGLIRDCKIEDIVDTAMPITICLAYFNCLNPLFYGLGKPKKYFLQLQLLYIPPKAKSH 327
QY 290 ---NKLKICSLKPKQPGHKTQRP 310
Db 328 SNLSTKMSTLSYRPSSENGNSSTKKP 352

RESULT 15
B41795
somatostatin receptor 2 - human
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: B41795
R:Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A:Title: Cloning and functional characterization of a family of human and mouse somatost
A:Reference number: A41795; MUID:92108031; PMID:1346068
A:Accession: B41795
A:Molecule type: DNA
A:Residues: 1-369 <YAM>
A:Cross-references: UNIPROT:P30874; GB:M81830; NID:g307435; PIDN:AAA58248.1; PID:g307436
A>Note: sequence extracted from NCBI backbone (NCBIN:74769, NCBIP:74770)
C:Genetics:
A:Gene: GDB:SSTR2
A:Cross-references: GDB:134186; OMIM:182452
A:Map position: 17q24-17q24

```

```

Db 279 VFVICWMPFYVQLVNVFAEQDDAT-----VSQLSVILGYANSKANPILYGLSDNFKR 332
QY 288 FYNKLKIC 295
Db 333 SFQRI-LC 339

RESULT 14
S15403
angiotensin II receptor type 1 - bovine
C:Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C:Accession: S15403
R:Sasaki, K.; Yamano, Y.; Bardhan, S.; Iwai, N.; Murray, J.J.; Hasegawa, M.; Matsuda, Y.
Nature 351, 230-233, 1991
A:Title: Cloning and expression of a complementary DNA encoding a bovine adrenal angioten
A:Reference number: S15403; MUID:91251900; PMID:2041569
A:Accession: S15403
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <SAS>
A:Cross-references: GB:X62294; NID:g43; PIDN:CAA44182.1; PID:g44
C:Superfamily: vertebrate rhodopsin

Query Match 16.4%; Score 304.5; DB 2; Length 359;
Best Local Similarity 24.9%; Pred. No. 2.8e-20;
Matches 81; Conservative 68; Mismatches 143; Indels 33; Gaps 8;

QY 17 VMPELLIVAFVLGALNGVALCGFCFHMKTWPKSTVYLFNLAVADPLLMICLPFRDYLL 76
Db 30 MIPTLYSIIFVVGIFGSLVIVIVFYMKLTVASVFLNLALADLCFLLTPLWAVTA 89
QY 77 RRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVPHPHVAINTISTRVAAGIV 136
Db 90 MEYRWPFNGVILCKIASASVSFNLYASVPLLCISIDRYLAIVHPMKS-RLRRTMLVAKVT 148
QY 137 C-TLWALVILGTVYLL-ENHLCVQETAVSCSFIMESANGMHDIMFOLE----FFMPL 189
Db 149 CIIWLLAGLASLPTIHRNVFFIENITITVCAPHYESQNSTLPVGLGLTKNLLGLFLPFF 208
QY 190 GIILFCSPKIVMSLRRRQQLARQARMKKATRFIMVVAIV--FITCYLP----SVSARLYF 243
Db 209 -LIILTSYLLWTKLKAYEIQKNPKRDKDIFKIILAIVLFFFSWVPHQITTFMDVLIQ 267
QY 244 LWTVPSSACDPSVHGALHITLSFTYMNMSMLDPLVYFSSPSPPKPY----- 289
Db 268 LGLIRDCKIEDIVDTAMPITICLAYFNCLNPLFYGLGKPKKYFLQLQLLYIPPKAKSH 327
QY 290 ---NKLKICSLKPKQPGHKTQRP 310
Db 328 SNLSTKMSTLSYRPSSENGNSSTKKP 352

RESULT 15
B41795
somatostatin receptor 2 - human
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: B41795
R:Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A:Title: Cloning and functional characterization of a family of human and mouse somatost
A:Reference number: A41795; MUID:92108031; PMID:1346068
A:Accession: B41795
A:Molecule type: DNA
A:Residues: 1-369 <YAM>
A:Cross-references: UNIPROT:P30874; GB:M81830; NID:g307435; PIDN:AAA58248.1; PID:g307436
A>Note: sequence extracted from NCBI backbone (NCBIN:74769, NCBIP:74770)
C:Genetics:
A:Gene: GDB:SSTR2
A:Cross-references: GDB:134186; OMIM:182452
A:Map position: 17q24-17q24

```


THIS PAGE BLANK (USE TO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2005, 18:25:17 ; Search time 43 Seconds
(without alignments)
600.665 Million cell updates/sec

Title: US-10-719-692-6
Perfect score: 1853
Sequence: 1 MTNGSCCRIGDTISQVMP.....ANSFOSQDQWDPHVEMH 346

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCFUS COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	881.5	47.6	387	4	US-09-170-496D-222
2	880.5	47.5	387	4	US-09-170-496D-108
3	880.5	47.5	387	4	US-09-944-807-21
4	529	28.5	423	2	US-08-955-713-2
5	510	27.5	476	2	US-08-955-713-4
6	451.5	24.4	319	3	US-09-130-749-2
7	451.5	24.4	319	3	US-09-130-749-2
8	448.5	24.2	319	4	US-09-170-496D-60
9	448.5	24.2	319	4	US-09-170-496D-196
10	371	20.0	362	3	US-08-513-974B-374
11	362.5	19.6	373	2	US-08-559-524A-4
12	362.5	19.6	373	3	US-08-749-707-4
13	362.5	19.6	373	4	US-09-947-922-4
14	361.5	19.5	346	4	US-09-585-876-2
15	354	19.1	373	4	US-09-745-842-14
16	346.5	18.7	370	3	US-08-781-250-2
17	336	18.1	339	1	US-08-153-848-44
18	336	18.1	339	2	US-08-812-871-3
19	336	18.1	339	3	US-09-299-843A-44
20	336	18.1	339	3	US-09-088-337B-44
21	336	18.1	339	4	US-09-170-496D-32
22	336	18.1	339	5	PCT-US93-11153-44
23	336	18.1	339	5	PCT-US95-07180-2
24	335	18.1	339	4	US-09-170-496D-182
25	328.5	17.7	302	2	US-08-467-948A-30
26	328.5	17.7	302	3	US-08-467-947A-30
27	327	17.6	309	3	US-09-422-869-20

28	325	17.5	344	2	US-08-467-948A-8	Sequence 8, Appli
29	325	17.5	344	3	US-08-467-947A-8	Sequence 8, Appli
30	315.5	17.0	374	4	US-09-102-710B-3	Sequence 3, Appli
31	314	16.9	373	3	US-08-513-974B-373	Sequence 373, App
32	308	16.6	325	1	US-08-118-270-51	Sequence 51, Appl
33	308	16.6	325	5	PCT-US93-08528-51	Sequence 51, Appl
34	307	16.6	391	1	US-07-816-283-4	Sequence 4, Appli
35	307	16.6	391	1	US-08-417-103-4	Sequence 4, Appli
36	307	16.6	395	1	US-08-097-938-5	Sequence 5, Appli
37	307	16.6	395	1	US-08-476-000-5	Sequence 5, Appli
38	307	16.6	395	1	US-08-472-840-5	Sequence 5, Appli
39	307	16.6	395	2	US-08-476-976-5	Sequence 5, Appli
40	307	16.6	395	3	US-08-474-410-5	Sequence 5, Appli
41	306	16.5	398	1	US-08-097-938-6	Sequence 6, Appli
42	306	16.5	398	1	US-08-476-000-6	Sequence 6, Appli
43	306	16.5	398	2	US-08-472-840-6	Sequence 6, Appli
44	306	16.5	398	2	US-08-476-976-6	Sequence 6, Appli
45	306	16.5	398	3	US-08-474-410-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-170-496D-222
; Sequence 222, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SEQ ID NO 222
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-222

Query Match	47.6%	Score 881.5	DB 4	Length 387
Best Local Similarity	52.2%	Pred. No. 5e-68		
Matches 178	Conservative 49	Mismatches 107	Indels 7	Gaps 4
QY	5	SCCRIGDTISQVMPPLIIVAFVLGALNGVALCGCFHMKTKPSTVYLFNLAVADFL 64		
DB	17	NCCVFRDDFIKVLPPVLGLEIFGLGLGLALWIFCFHLKSKWSRIFLNLAVADFL 76		
QY	65	MTCLPFRDYYLRRHNAFGDIPCRVGLFTLMMNRAGSIVFTVVAADRYFKVVPHPH 124		
DB	77	IICLPFWMYVYRRSDWKPGDIPCLRLVLFMFAMNRQSGIIFLTWAVDRYFRVHPH 136		
QY	125	NTISRTVAAGIVCTIHALVILGTVYLLLENHLCVQETAVSCSFIMESANGHMDIMF 184		
DB	137	NKISNTAAITSCLLMGITVGLTVHLLKKGLIQNGPANVCISFICHTFRWHEAMFL 196		
QY	185	FWPGLIILFCFSKIVLSRRRQQLARQRMKATRFIMVAIVFITCVLPVSARLYFL 244		
DB	197	FLPLGLIILFCSARIINLSLRQ-QMDRAKIKRATFIMVAIVFICLPVSVVIRIF 255		
QY	245	WTVPSSA---CD--PSVHGALHITISFTYMSMLDPLVYFSSPFPKYNKIKTCSL 299		
DB	256	WLHSTSGTQNCVYRSDVLAFFITLSFTYMSMLDPLVYFSSPFPFPFSTLINRCL 315		
QY	300	KPGHSTQRPPEMIPISNLGRSCISVANSFOSQDQWD 340		
DB	316	KMTGPDPNNRSTSVELTDPNKT-RGAPEALMANSCEPWS 355		

RESULT 2
US-09-170-496D-108
; Sequence 108, Application US/09170496D
; Patent No. 655339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: NO. 655339-Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-108

Query Match 47.5%; Score 880.5; DB 4; Length 387;
Best Local Similarity 52.2%; Pred. No. 6.1e-68;
Matches 178; Conservative 49; Mismatches 107; Indels 7; Gaps 4;
QY 5 SCRIEGDTISQVMPPLLIIVAFVLGALNGVALCGFCFHMKTWKPSTVYLFNLAVADFLL 64
DB 17 NCCVFRDDFTAKVLPVVLGLEIFGLLGNGLALWIFCFHLKSWKSSRIPLFNLAVADFLL 76
QY 65 MICLPRDTYYLRRRHAFGDI PCRVGLFTLAMNAGSIVFTVVAADRYFKVHPPHAY 124
DB 77 IICLPFVMDYYVRRSDWNGDIPCRVLFPFAMNRQGSIIIFLTVAADRYFKVHPPHAY 136
QY 125 NTISTRVAAIGVCTLWALVILGTVLLLENHLCVQETAVSCSFIMESANGWHDIMFOLE 184
DB 137 NKISNWTAAIISCLLWGTVGLTVHLLKKLLIQNGPANVCISFSICHTFRWHEAMFLE 196
QY 185 FFMPLGIILFCFSKIVMSLRRQOLARQARKKATFRFMVAIVTICVLPVSARLYPL 244
DB 197 FLLPLGIILFCSARIISLRQ-QMDRHAKIKRAITFMVAIVFVICFLPSVVVRIRIF 255
QY 245 WTVPSA---CD--PSVHGALHITLSFTYMNMLDPLVYFSSPSFPKFKYKLCISLKP 299
DB 256 WLLHTSGTQNCVYRSVDLAFITLSFTYMNMLDPLVYFSSPSFPNFFSTLINRCLQR 315
QY 300 KQPGHKTQRPPEMPISNLGRSCISVANSFQSDGQWDP 340
DB 316 KMTGEPDNNRSTVELTGDPNKT-RGAPEALMANGEPWSP 355

RESULT 3
US-09-944-807-21
; Sequence 21, Application US/09944807
; Patent No. 6773895
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim Pharma KG
; TITLE OF INVENTION: Method for identifying substances which positively
; TITLE OF INVENTION: influence inflammatory conditions of chronic
; TITLE OF INVENTION: inflammatory airway diseases
; FILE REFERENCE: 082.00n
; CURRENT APPLICATION NUMBER: US/09/944,807
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: UK 0021484.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-944-807-21
Query Match 47.5%; Score 880.5; DB 4; Length 387;

Best Local Similarity 52.2%; Pred. No. 6.1e-68;
Matches 178; Conservative 49; Mismatches 107; Indels 7; Gaps 4;
QY 5 SCRIEGDTISQVMPPLLIIVAFVLGALNGVALCGFCFHMKTWKPSTVYLFNLAVADFLL 64
DB 17 NCCVFRDDFTAKVLPVVLGLEIFGLLGNGLALWIFCFHLKSWKSSRIPLFNLAVADFLL 76
QY 65 MICLPRDTYYLRRRHAFGDI PCRVGLFTLAMNAGSIVFTVVAADRYFKVHPPHAY 124
DB 77 IICLPFVMDYYVRRSDWNGDIPCRVLFPFAMNRQGSIIIFLTVAADRYFKVHPPHAY 136
QY 125 NTISTRVAAIGVCTLWALVILGTVLLLENHLCVQETAVSCSFIMESANGWHDIMFOLE 184
DB 137 NKISNWTAAIISCLLWGTVGLTVHLLKKLLIQNGPANVCISFSICHTFRWHEAMFLE 196
QY 185 FFMPLGIILFCFSKIVMSLRRQOLARQARKKATFRFMVAIVTICVLPVSARLYPL 244
DB 197 FLLPLGIILFCSARIISLRQ-QMDRHAKIKRAITFMVAIVFVICFLPSVVVRIRIF 255
QY 245 WTVPSA---CD--PSVHGALHITLSFTYMNMLDPLVYFSSPSFPKFKYKLCISLKP 299
DB 256 WLLHTSGTQNCVYRSVDLAFITLSFTYMNMLDPLVYFSSPSFPNFFSTLINRCLQR 315
QY 300 KQPGHKTQRPPEMPISNLGRSCISVANSFQSDGQWDP 340
DB 316 KMTGEPDNNRSTVELTGDPNKT-RGAPEALMANGEPWSP 355

RESULT 4
US-08-955-713-2
; Sequence 2, Application US/08955713
; Patent No. 5955308
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: MOONEY, JEFFREY
; APPLICANT: BERGSM, DERK
; APPLICANT: HALSEA, WENDY
; TITLE OF INVENTION: CDNA CLONE HEAD54 THAT ENCODES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955.713
; FILING DATE: 23-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,124
; FILING DATE: 18-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 423 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
A HUMAN 7-TRANS

Db 327 ATRKSSRRSEP--NVQSKSEMTLNIL 351

RESULT 11
US-08-559-524A-4
; Sequence 4, Application US/08559524A
; Patent No. 5871963
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,524A
; FILING DATE: 15-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044481-5010-00-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 373 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-559-524A-4

Query Match 19.6%; Score 362.5; DB 2; Length 373;
Best Local Similarity 27.5%; Pred. No. 2e-23;
Matches 92; Conservative 68; Mismatches 140; Indels 35; Gaps 7;
QY 18 MPPLLI VAVL GNGV ALCG FCFH MKTKPSTVYLFNLAVADFLMLCLPFRDYLYR 77
Db 54 LPVYILVFIIGLGN SVAIWV FVHKPWSGISVYMFNLALADFLYVLTLPALIFYPN 113
QY 78 RRHWAFGDIPCRVGLFTLAMNRAGSIVELTVVAADRYFKVPHHVAVNTISTRVAAGIVC 137
Db 114 KTDWIFGDAMCKLQRFIFHNLYGSILFTCTISAHRYSGVYVPLKSLGRKKKNVYISV 173
QY 138 TLWALVILGTVYLLLENHLCVQET-AVSC-----ESFTMESANGWHDIMFQLEPFM 187
Db 174 LWLILVVGISPLFYSGTGIRKNTITCYDTSDEYLSYFIYSM-----CTTVAMFCV 228
QY 188 PLGIILFCSEKIVMSLRRLRQOLARQARKKATRFIMVVAIVITCYLP-----SVSAR 240
Db 229 PLVILIGCYGLIVRALIYK-DLDNSPLRRKSIYLVIIIVTVFAVSIYIPFHVMTNLRAR 287
QY 241 LYFLWTVPSSACDPSVHGALHITLSFTYMSMLDPLVYFSSPFPKFNKLIKICSLKPK 300
Db 288 LDF-QTPWCAFNDRVYATYQVTRGLASLNSCVDPIYFLAGDTFRRLSR-----337
QY 301 QGHKSKTQRPBEMPIISNLGRSCISVANSFQSQSD 335
Db 338 --ATRKASRRSEANLQSKSEMTLNILSEFKQNGD 370

RESULT 12
US-08-749-707-4
; Sequence 4, Application US/08749707
; Patent No. 6063582
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,707
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044481-5010-01-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 373 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-749-707-4

Query Match 19.6%; Score 362.5; DB 3; Length 373;
Best Local Similarity 27.5%; Pred. No. 2e-23;
Matches 92; Conservative 68; Mismatches 140; Indels 35; Gaps 7;
QY 18 MPPLLI VAVL GNGV ALCG FCFH MKTKPSTVYLFNLAVADFLMLCLPFRDYLYR 77
Db 54 LPVYILVFIIGLGN SVAIWV FVHKPWSGISVYMFNLALADFLYVLTLPALIFYPN 113
QY 78 RRHWAFGDIPCRVGLFTLAMNRAGSIVELTVVAADRYFKVPHHVAVNTISTRVAAGIVC 137
Db 114 KTDWIFGDAMCKLQRFIFHNLYGSILFTCTISAHRYSGVYVPLKSLGRKKKNVYISV 173
QY 138 TLWALVILGTVYLLLENHLCVQET-AVSC-----ESFTMESANGWHDIMFQLEPFM 187
Db 174 LWLILVVGISPLFYSGTGIRKNTITCYDTSDEYLSYFIYSM-----CTTVAMFCV 228
QY 188 PLGIILFCSEKIVMSLRRLRQOLARQARKKATRFIMVVAIVITCYLP-----SVSAR 240
Db 229 PLVILIGCYGLIVRALIYK-DLDNSPLRRKSIYLVIIIVTVFAVSIYIPFHVMTNLRAR 287
QY 241 LYFLWTVPSSACDPSVHGALHITLSFTYMSMLDPLVYFSSPFPKFNKLIKICSLKPK 300
Db 288 LDF-QTPWCAFNDRVYATYQVTRGLASLNSCVDPIYFLAGDTFRRLSR-----337
QY 301 QGHKSKTQRPBEMPIISNLGRSCISVANSFQSQSD 335
Db 338 --ATRKASRRSEANLQSKSEMTLNILSEFKQNGD 370

RESULT 13
US-09-947-922-4


```
; FEATURE:
; OTHER INFORMATION: P2Y1 purinergic receptor; p2yr
US-09-745-842-14

Query Match      19.1%; Score 354; DB 4; Length 373;
Best Local Similarity 29.2%; Pred. No. 1.1e-22;
Matches 93; Conservative 66; Mismatches 132; Indels 28; Gaps 8;

QY 18 MEPLLIIVAVLGGALGVALGCPCHMKTKPESTVYLENLAADLMLICLPFRDYYLR 77
Db 54 LPAVYILVFIIGFLGNSVAIMWFVFMKFPWGSIGSYMENLADFLYVTLTPALIFYFN 113

QY 78 RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVAAADRYFKVPHPHAVNTISTRVAAGIVC 137
Db 114 KTDWIFGDAMCKLQRFIFHVNLYGSILFELTCISAHRYSGVYVPLKSLGRKKNAICISV 173

QY 138 TLWALVILGTVYLLLENHLCVOET-AVSC-----ESFTMESANGWHDIMFOLEPFM 187
Db 174 LVMLIIVWVAISPILFYSGTGVKKNKTIITCYDTTSDYLRSYFIYSM-----CTTVAMFCV 228

QY 188 PLGIILFCGSKIVWSLRRQQLARQARMKKATRFIMVVAIVEITCYLP-----SVSAR 240
Db 229 PLVLIIGCYGLIVRALIYK-DLDNSPLRRKSYLVIIIVLTVFAVSIIPIFHVMTNLRAR 287

QY 241 LVFLWTVPSACDPSVHGALHITLSFTVMNSMLDPLVYFFSSPSPKFNKIKICSLKPK 300
Db 288 LDF-QTPAMCAFNDRVYATYQVTRGLASLNSCVDPIILYFLAGDTFPR---RLSRATRKAS 343

QY 301 QFGHSKTQ-RPEEMPISNL 318
Db 344 RREANLQSKSEDWTLNIL 362
```

Search completed: August 30, 2005, 18:35:23
Job time : 45 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2005, 18:28:13 ; Search time 162 Seconds
(without alignments)
839.213 Million cell updates/sec

Title: US-10-719-692-6
Perfect score: 1853
Sequence: 1 MYNGSCCRIEGDTISQVMP...ANFSQSDGQWDHIVEWH 346

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1767149 seqs, 392926209 residues

Total number of hits satisfying chosen parameters: 1767149

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*

20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*

21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1853	100.0	346	9	US-09-862-274-2
2	1853	100.0	346	9	US-09-942-374-2
3	1853	100.0	346	10	US-09-886-041-2
4	1853	100.0	346	10	US-09-782-974C-80
5	1853	100.0	346	14	US-10-188-149A-2
6	1853	100.0	346	14	US-10-079-384-18
7	1853	100.0	346	14	US-10-240-842-2
8	1853	100.0	346	14	US-10-225-567A-668
9	1853	100.0	346	14	US-10-201-481-7
10	1853	100.0	346	14	US-10-278-141-3
11	1853	100.0	346	14	US-10-321-807-24

12	1853	100.0	346	14	US-10-076-260-2
13	1853	100.0	346	14	US-10-044-643-2
14	1853	100.0	346	15	US-10-296-081-3
15	1853	100.0	346	15	US-10-210-172-178
16	1853	100.0	346	15	US-10-210-172-184
17	1853	100.0	346	15	US-10-210-172-188
18	1853	100.0	346	15	US-10-343-650A-8
19	1853	100.0	346	15	US-10-665-956-2
20	1853	100.0	346	15	US-10-332-032-1
21	1853	100.0	346	16	US-10-321-807-24
22	1853	100.0	346	16	US-10-314-048A-24
23	1853	100.0	346	16	US-10-482-151-6
24	1853	100.0	346	17	US-10-897-815-24
25	1853	100.0	346	17	US-10-635-398-78
26	1853	100.0	346	17	US-10-635-398-82
27	1853	100.0	346	17	US-10-635-398-90
28	1853	100.0	346	17	US-10-467-492A-80
29	1853	100.0	346	17	US-10-975-979-80
30	1853	100.0	346	18	US-10-930-662-24
31	1853	100.0	352	15	US-10-210-172-192
32	1853	100.0	584	17	US-10-505-486-88
33	1849	99.8	346	14	US-10-094-417-8
34	1849	99.8	346	20	US-11-086-846-8
35	1848	99.7	345	17	US-10-635-398-94
36	1846	99.6	346	15	US-10-210-172-180
37	1846	99.6	346	17	US-10-635-398-84
38	1839	99.2	346	14	US-10-044-643-5
39	1839	99.2	346	15	US-10-210-172-182
40	1839	99.2	346	17	US-10-635-398-86
41	1739	93.8	342	14	US-10-092-135-2
42	1686	91.0	314	15	US-10-210-172-186
43	1686	91.0	314	17	US-10-635-398-88
44	1686	91.0	320	15	US-10-210-172-190
45	1686	91.0	320	15	US-10-210-172-194

ALIGNMENTS

RESULT 1

US-09-862-274-2

; Sequence 2, Application US/09862274

; Patent No. US2002005202A1

; GENERAL INFORMATION:

; APPLICANT: ELSHOURBAGY, NABIL

; APPLICANT: GATTU, MAHANANDESHWAR

; APPLICANT: SHABON, USMAN

; APPLICANT: IGNAR, DIANE MICHELE

; TITLE OF INVENTION: MOLECULAR CLONING OF A CHEMOKINE LIKE

; TITLE OF INVENTION: 7TMR (AXOR87)

; FILE REFERENCE: GP-70703-1

; CURRENT APPLICATION NUMBER: US/09/862,274

; CURRENT FILING DATE: 2001-05-22

; PRIOR APPLICATION NUMBER: US 09/580,675

; PRIOR FILING DATE: 2000-05-30

; PRIOR APPLICATION NUMBER: GB 0026839.1

; PRIOR FILING DATE: 2000-11-02

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 346

; TYPE: PRT

; ORGANISM: HOMO SAPIENS

US-09-862-274-2

Query Match 100.0%; Score 1853; DB 9; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.6e-163;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNGSCCRIEGDTISQVMPPLIVAFVILGALNGVALGCGCFHMTKWPSTVYLFNLAVA 60
|||||

Db 1 MYNGSCCRIEGDTISQVMPPLIVAFVILGALNGVALGCGCFHMTKWPSTVYLFNLAVA 60
|||||

```
QY 61 DFLLMICLPFRDYLLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHP 120
Db 61 DFLLMICLPFRDYLLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHP 120
QY 121 HAVNTISTRVAAGIVCTLMALVILGTVYLLLENHLCVQETA VCSFIMESANGWHIM 180
Db 121 HAVNTISTRVAAGIVCTLMALVILGTVYLLLENHLCVQETA VCSFIMESANGWHIM 180
QY 181 FOLEFMPGLGILFCSFKIVSLRRRQQLARQARKKATRFIMVAIVFITCYLPSVSAR 240
Db 181 FOLEFMPGLGILFCSFKIVSLRRRQQLARQARKKATRFIMVAIVFITCYLPSVSAR 240
QY 241 LYFLMTVPSSACDPSVHGALHTLSTFTYNSMLDPLVYFSSPPKFNKIKICSLKPK 300
Db 241 LYFLMTVPSSACDPSVHGALHTLSTFTYNSMLDPLVYFSSPPKFNKIKICSLKPK 300
QY 301 QPGHSKTQRPPEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346
Db 301 QPGHSKTQRPPEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346
```

RESULT 2

```
US-09-942-374-2
; Sequence 2, Application US/09942374
; Patent No. US20020137063A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Gimeno, Ruth
; APPLICANT: White, David
; TITLE OF INVENTION: 57242, a Human G-Protein Coupled
; FILE REFERENCE: MP12000-368PIR
; CURRENT APPLICATION NUMBER: US/09/942,374
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 60/228,409
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: human
US-09-942-374-2
```

```
Query Match 100.0%; Score 1853; DB 9; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.6e-163;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MYNGSCCRLEGDTISQVMPPLLIIVAFVLGALNGVALCGCFHMKTKPSTVYLFNLAVA 60
Db 1 MYNGSCCRLEGDTISQVMPPLLIIVAFVLGALNGVALCGCFHMKTKPSTVYLFNLAVA 60
QY 61 DFLLMICLPFRDYLLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHP 120
Db 61 DFLLMICLPFRDYLLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHP 120
QY 121 HAVNTISTRVAAGIVCTLMALVILGTVYLLLENHLCVQETA VCSFIMESANGWHIM 180
Db 121 HAVNTISTRVAAGIVCTLMALVILGTVYLLLENHLCVQETA VCSFIMESANGWHIM 180
QY 181 FOLEFMPGLGILFCSFKIVSLRRRQQLARQARKKATRFIMVAIVFITCYLPSVSAR 240
Db 181 FOLEFMPGLGILFCSFKIVSLRRRQQLARQARKKATRFIMVAIVFITCYLPSVSAR 240
QY 241 LYFLMTVPSSACDPSVHGALHTLSTFTYNSMLDPLVYFSSPPKFNKIKICSLKPK 300
Db 241 LYFLMTVPSSACDPSVHGALHTLSTFTYNSMLDPLVYFSSPPKFNKIKICSLKPK 300
QY 301 QPGHSKTQRPPEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346
Db 301 QPGHSKTQRPPEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346
```

```
RESULT 3
US-09-886-041-2
; Sequence 2, Application US/09886041
; Publication No. US20030059869A1
; GENERAL INFORMATION:
; APPLICANT: XIA, TAI-HE
; APPLICANT: NI, DONGHUI
; APPLICANT: EISHINGDELO, HAIFENG
; APPLICANT: ARDATI, ALI
; APPLICANT: MINNICH, ANNE
; APPLICANT: JUPP, RAY
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 41491
; CURRENT APPLICATION NUMBER: US/09/886,041
; CURRENT FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-886-041-2
```

```
Query Match 100.0%; Score 1853; DB 10; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.6e-163;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYNGSCCRLEGDTISQVMPPLLIIVAFVLGALNGVALCGCFHMKTKPSTVYLFNLAVA 60
Db 1 MYNGSCCRLEGDTISQVMPPLLIIVAFVLGALNGVALCGCFHMKTKPSTVYLFNLAVA 60
QY 61 DFLLMICLPFRDYLLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHP 120
Db 61 DFLLMICLPFRDYLLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHP 120
QY 121 HAVNTISTRVAAGIVCTLMALVILGTVYLLLENHLCVQETA VCSFIMESANGWHIM 180
Db 121 HAVNTISTRVAAGIVCTLMALVILGTVYLLLENHLCVQETA VCSFIMESANGWHIM 180
QY 181 FOLEFMPGLGILFCSFKIVSLRRRQQLARQARKKATRFIMVAIVFITCYLPSVSAR 240
Db 181 FOLEFMPGLGILFCSFKIVSLRRRQQLARQARKKATRFIMVAIVFITCYLPSVSAR 240
QY 241 LYFLMTVPSSACDPSVHGALHTLSTFTYNSMLDPLVYFSSPPKFNKIKICSLKPK 300
Db 241 LYFLMTVPSSACDPSVHGALHTLSTFTYNSMLDPLVYFSSPPKFNKIKICSLKPK 300
QY 301 QPGHSKTQRPPEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346
Db 301 QPGHSKTQRPPEMPISNLGRSCISVANSFQSDGQWDPHIVEWH 346
```

RESULT 4

```
US-09-782-974C-80
; Sequence 80, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: No. US20030082534A1el G Protein Coupled Receptor
; FILE REFERENCE: 411USPHRM311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; PRIOR FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
```

```
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-782-974C-80

Query Match      100.0%; Score 1853; DB 10; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.6e-163;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNSCCRIEGDTISQVMPPLIIVAFVLGALNGVALCGFCFHMKTWKPSVTLFNLAVA 60
DB 1 MYNSCCRIEGDTISQVMPPLIIVAFVLGALNGVALCGFCFHMKTWKPSVTLFNLAVA 60

QY 61 DFLLMICLPFRDYYLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHP 120
DB 61 DFLLMICLPFRDYYLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHP 120

QY 121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180
DB 121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180

QY 181 FOLEPFMPLGIILFCSFKIVNSLRRLRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
DB 181 FOLEPFMPLGIILFCSFKIVNSLRRLRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

QY 241 LYFLMTVPSSACDPSVHGALHITLSFTYNSMLDPLVYFSSPPKPKFNKLIKISLKP 300
DB 241 LYFLMTVPSSACDPSVHGALHITLSFTYNSMLDPLVYFSSPPKPKFNKLIKISLKP 300

QY 301 QPGHKTQRPPEMPTISNLGRSCISVANSFQSDGQWDPHIVEWH 346
DB 301 QPGHKTQRPPEMPTISNLGRSCISVANSFQSDGQWDPHIVEWH 346

; US-10-188-149A-2
; Sequence 2, Application US/10188149A
; Publication No. US2003007734A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000782-CON
; CURRENT APPLICATION NUMBER: US/10/188,149A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 09/666,535
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US 60/230,459
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: US 60/192,419
; PRIOR FILING DATE: 2000-03-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
; US-10-188-149A-2

Query Match      100.0%; Score 1853; DB 14; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.6e-163;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNSCCRIEGDTISQVMPPLIIVAFVLGALNGVALCGFCFHMKTWKPSVTLFNLAVA 60
DB 1 MYNSCCRIEGDTISQVMPPLIIVAFVLGALNGVALCGFCFHMKTWKPSVTLFNLAVA 60

QY 61 DFLLMICLPFRDYYLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHP 120
DB 61 DFLLMICLPFRDYYLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHP 120

QY 121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180
DB 121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180

QY 181 FOLEPFMPLGIILFCSFKIVNSLRRLRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
DB 181 FOLEPFMPLGIILFCSFKIVNSLRRLRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

QY 241 LYFLMTVPSSACDPSVHGALHITLSFTYNSMLDPLVYFSSPPKPKFNKLIKISLKP 300
DB 241 LYFLMTVPSSACDPSVHGALHITLSFTYNSMLDPLVYFSSPPKPKFNKLIKISLKP 300

QY 301 QPGHKTQRPPEMPTISNLGRSCISVANSFQSDGQWDPHIVEWH 346
DB 301 QPGHKTQRPPEMPTISNLGRSCISVANSFQSDGQWDPHIVEWH 346

; US-10-079-384-18
; Sequence 18, Application US/10079384
; Publication No. US2003010896A1
; GENERAL INFORMATION:
; APPLICANT: Communi, Didier
; TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 9409/2132
; CURRENT APPLICATION NUMBER: US/10/079,384
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/885,453
; PRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-079-384-18

Query Match      100.0%; Score 1853; DB 14; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.6e-163;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNSCCRIEGDTISQVMPPLIIVAFVLGALNGVALCGFCFHMKTWKPSVTLFNLAVA 60
DB 1 MYNSCCRIEGDTISQVMPPLIIVAFVLGALNGVALCGFCFHMKTWKPSVTLFNLAVA 60

QY 61 DFLLMICLPFRDYYLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHP 120
DB 61 DFLLMICLPFRDYYLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHP 120

QY 121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180
DB 121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180

QY 181 FOLEPFMPLGIILFCSFKIVNSLRRLRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
DB 181 FOLEPFMPLGIILFCSFKIVNSLRRLRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

QY 241 LYFLMTVPSSACDPSVHGALHITLSFTYNSMLDPLVYFSSPPKPKFNKLIKISLKP 300
DB 241 LYFLMTVPSSACDPSVHGALHITLSFTYNSMLDPLVYFSSPPKPKFNKLIKISLKP 300

; RESULT 6
; US-10-079-384-18
; Sequence 18, Application US/10079384
; Publication No. US2003010896A1
; GENERAL INFORMATION:
; APPLICANT: Communi, Didier
; TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 9409/2132
; CURRENT APPLICATION NUMBER: US/10/079,384
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/885,453
; PRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-079-384-18
```

|||||
Db 241 LYFLMTVPSSACDPSVHGALHITLSTYMNMLDPLVYFSSPPKFNKIKICSLKPK 300
QY 301 QPGHSKTQRPPEMPIISNLGRRSCISVANSFQSDGQWDPHIVEWH 346
Db 301 QPGHSKTQRPPEMPIISNLGRRSCISVANSFQSDGQWDPHIVEWH 346

RESULT 7
US-10-240-842-2
; Sequence 2, Application US/10240842
; Publication No. US20030109673A1
; GENERAL INFORMATION:
; APPLICANT: Xiao Yonghong
; TITLE OF INVENTION: REGULATION OF HUMAN HM74-LIKE G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 4974.00883
; CURRENT APPLICATION NUMBER: US/10/240,842
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 60/194,701
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-240-842-2

Query Match 100.0%; Score 1853; DB 14; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.6e-163;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNGSCCRIEGDTISQVMPPLLIIVAFVLGALNGVALCGFCFHMKTWKPSVTYLFNLAVA 60
Db 1 MYNGSCCRIEGDTISQVMPPLLIIVAFVLGALNGVALCGFCFHMKTWKPSVTYLFNLAVA 60
QY 61 DFLMCLCPFRDYLLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYPKVHP 120
Db 61 DFLMCLCPFRDYLLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYPKVHP 120
QY 121 HAVNTISTRVAAGIVCTLMALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180
Db 121 HAVNTISTRVAAGIVCTLMALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180
QY 181 FOLEFFMPLGIILFCSPKIVMSLRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
Db 181 FOLEFFMPLGIILFCSPKIVMSLRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
QY 241 LYFLMTVPSSACDPSVHGALHITLSTYMNMLDPLVYFSSPPKFNKIKICSLKPK 300
Db 241 LYFLMTVPSSACDPSVHGALHITLSTYMNMLDPLVYFSSPPKFNKIKICSLKPK 300
QY 301 QPGHSKTQRPPEMPIISNLGRRSCISVANSFQSDGQWDPHIVEWH 346
Db 301 QPGHSKTQRPPEMPIISNLGRRSCISVANSFQSDGQWDPHIVEWH 346

RESULT 8
US-10-225-567A-668
; Sequence 668, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: Patentin version 3.1
; SEQ ID NO 668
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-668

Query Match 100.0%; Score 1853; DB 14; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.6e-163;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYNGSCCRIEGDTISQVMPPLLIIVAFVLGALNGVALCGFCFHMKTWKPSVTYLFNLAVA 60
Db 1 MYNGSCCRIEGDTISQVMPPLLIIVAFVLGALNGVALCGFCFHMKTWKPSVTYLFNLAVA 60
QY 61 DFLMCLCPFRDYLLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYPKVHP 120
Db 61 DFLMCLCPFRDYLLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYPKVHP 120
QY 121 HAVNTISTRVAAGIVCTLMALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180
Db 121 HAVNTISTRVAAGIVCTLMALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180
QY 181 FOLEFFMPLGIILFCSPKIVMSLRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
Db 181 FOLEFFMPLGIILFCSPKIVMSLRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
QY 241 LYFLMTVPSSACDPSVHGALHITLSTYMNMLDPLVYFSSPPKFNKIKICSLKPK 300
Db 241 LYFLMTVPSSACDPSVHGALHITLSTYMNMLDPLVYFSSPPKFNKIKICSLKPK 300
QY 301 QPGHSKTQRPPEMPIISNLGRRSCISVANSFQSDGQWDPHIVEWH 346
Db 301 QPGHSKTQRPPEMPIISNLGRRSCISVANSFQSDGQWDPHIVEWH 346

RESULT 9
US-10-201-481-7
; Sequence 7, Application US/10201481
; Publication No. US20030119024A1
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Biery, Matthew
; TITLE OF INVENTION: Genes and Proteins Associated with T-Cell Activation
; FILE REFERENCE: 9301-133-999
; CURRENT APPLICATION NUMBER: US/10/201,481
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,968
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-481-7

Query Match 100.0%; Score 1853; DB 14; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.6e-163;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYNGSCCRIEGDTISQVMPPLLIIVAFVLGALNGVALCGFCFHMKTWKPSVTYLFNLAVA 60
Db 1 MYNGSCCRIEGDTISQVMPPLLIIVAFVLGALNGVALCGFCFHMKTWKPSVTYLFNLAVA 60
QY 61 DFLMCLCPFRDYLLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYPKVHP 120
Db 61 DFLMCLCPFRDYLLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYPKVHP 120
QY 121 HAVNTISTRVAAGIVCTLMALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180
Db 121 HAVNTISTRVAAGIVCTLMALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180

```
QY 181 FOLEFMPGILFCSFKIWSLRRRQQLARQARMKATRFIMVVAIVFITCYLPSVSAR 240
|
Db 181 FOLEFMPGILFCSFKIWSLRRRQQLARQARMKATRFIMVVAIVFITCYLPSVSAR 240
|
QY 241 LYFLMTVPSSACDPSVHGALHITLSFTYNSMLDPLVYFSSPPKPFYNKLIKCSLKP 300
|
Db 241 LYFLMTVPSSACDPSVHGALHITLSFTYNSMLDPLVYFSSPPKPFYNKLIKCSLKP 300
|
QY 301 QPGHKTQRPPEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
|
Db 301 QPGHKTQRPPEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
|
RESULT 10
US-10-278-141-3
; Sequence 3, Application US/10278141
; Publication No. US20030138818A1
; GENERAL INFORMATION:
; APPLICANT: PATTERSON, Chandra
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: THORNTON, Michael
; APPLICANT: LU, Yan
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: GRAUL, Richard
; APPLICANT: KHAN, Farrah A.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: WALIA, Narinder K.
; APPLICANT: NGUYEN, Dannel B.
; APPLICANT: YUE, Henry
; APPLICANT: HAFALIA, April
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: LAL, Preeti
; APPLICANT: REDDY, Roopa
; APPLICANT: KALLICK, Deborah A.
; APPLICANT: TANG, Y. Tom
; APPLICANT: AU-YOUNG, Janice
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0096 USA
; CURRENT APPLICATION NUMBER: US/10/278,141
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: 60/208,834
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/207,566
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US01/16285
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/205,628
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 60/208,861
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/206,222
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030138818A1 7474846CD1
US-10-278-141-3
```

```
Query Match 100.0%; Score 1853; DB 14; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.6e-163;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNSCCRIEGDTISQVMPPLIIVAFVLGALNGVALCGFCFHMKTWKPESTVYLFNLAVA 60
|
Db 1 MYNSCCRIEGDTISQVMPPLIIVAFVLGALNGVALCGFCFHMKTWKPESTVYLFNLAVA 60
|
QY 61 DFLLMICLPFRDYLLRRRHWAFGDI PCRVGLFTLAMNRAGSIVFLTVAADRYFKVHP 120
|
```

```
Db 61 DFLLMICLPFRDYLLRRRHWAFGDI PCRVGLFTLAMNRAGSIVFLTVAADRYFKVHP 120
|
QY 121 HVAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180
|
Db 121 HVAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180
|
QY 181 FOLEFMPGILFCSFKIWSLRRRQQLARQARMKATRFIMVVAIVFITCYLPSVSAR 240
|
Db 181 FOLEFMPGILFCSFKIWSLRRRQQLARQARMKATRFIMVVAIVFITCYLPSVSAR 240
|
QY 241 LYFLMTVPSSACDPSVHGALHITLSFTYNSMLDPLVYFSSPPKPFYNKLIKCSLKP 300
|
Db 241 LYFLMTVPSSACDPSVHGALHITLSFTYNSMLDPLVYFSSPPKPFYNKLIKCSLKP 300
|
QY 301 QPGHKTQRPPEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
|
Db 301 QPGHKTQRPPEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
|
RESULT 11
US-10-321-807-24
; Sequence 24, Application US/10321807
; Publication No. US20030166148A1
; GENERAL INFORMATION:
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Rupong
; APPLICANT: Lowitz, Kevin P.
; TITLE OF INVENTION: No. US20030166148A1-Endogenous, Constitutively Activated Human G
; FILE REFERENCE: AREN0086
; CURRENT APPLICATION NUMBER: US/10/321,807
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US/09/714,008
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,088
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,099
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,369
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/171,902
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,901
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,900
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/181,749
; PRIOR FILING DATE: 2000-02-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-321-807-24
```

```
Query Match 100.0%; Score 1853; DB 14; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.6e-163;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNSCCRIEGDTISQVMPPLIIVAFVLGALNGVALCGFCFHMKTWKPESTVYLFNLAVA 60
|
Db 1 MYNSCCRIEGDTISQVMPPLIIVAFVLGALNGVALCGFCFHMKTWKPESTVYLFNLAVA 60
|
QY 61 DFLLMICLPFRDYLLRRRHWAFGDI PCRVGLFTLAMNRAGSIVFLTVAADRYFKVHP 120
|
Db 61 DFLLMICLPFRDYLLRRRHWAFGDI PCRVGLFTLAMNRAGSIVFLTVAADRYFKVHP 120
|
```

QY 121 HAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180
DB 121 HAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180
QY 181 FOLEPFMPILGILFCFSFKIWSLRRRQQLARQARKKATRFIMVAIVFITCYLPSVSAR 240
DB 181 FOLEPFMPILGILFCFSFKIWSLRRRQQLARQARKKATRFIMVAIVFITCYLPSVSAR 240
QY 241 LYFLMTVPSSACDPSVHGALHITLSTFTYNSMLDPLVYFSSPPKFNKLIKSLKPK 300
DB 241 LYFLMTVPSSACDPSVHGALHITLSTFTYNSMLDPLVYFSSPPKFNKLIKSLKPK 300
QY 301 QPGHKTQRPPEMPISNLGRRSCISVANSFQSDGQMDPHIVEWH 346
DB 301 QPGHKTQRPPEMPISNLGRRSCISVANSFQSDGQMDPHIVEWH 346

RESULT 12

US-10-076-260-2
; Sequence 2, Application US/10076260
; Publication No. US20030171541A1
; GENERAL INFORMATION:
; APPLICANT: Elliott, Steven G.
; APPLICANT: Rogers, No. US20030171541A1ma
; APPLICANT: Busse, Leigh Anne
; TITLE OF INVENTION: G-Protein Coupled Receptor Molecules and Uses Thereof
; FILE REFERENCE: 02-076
; CURRENT APPLICATION NUMBER: US/10/076,260
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/269,040
; PRIOR FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-076-260-2

Query Match 100.0%; Score 1853; DB 14; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.6e-163;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNGSCCRIEGDTISQVMPPLLIIVAFVLGALNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
DB 1 MYNGSCCRIEGDTISQVMPPLLIIVAFVLGALNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
QY 61 DFLLMICLPFRDYYLRRHHWAFGDI PCRVGLFTLAMNRAGSIVFLTVVAADRYPKVVHP 120
DB 61 DFLLMICLPFRDYYLRRHHWAFGDI PCRVGLFTLAMNRAGSIVFLTVVAADRYPKVVHP 120
QY 121 HAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180
DB 121 HAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180
QY 181 FOLEPFMPILGILFCFSFKIWSLRRRQQLARQARKKATRFIMVAIVFITCYLPSVSAR 240
DB 181 FOLEPFMPILGILFCFSFKIWSLRRRQQLARQARKKATRFIMVAIVFITCYLPSVSAR 240
QY 241 LYFLMTVPSSACDPSVHGALHITLSTFTYNSMLDPLVYFSSPPKFNKLIKSLKPK 300
DB 241 LYFLMTVPSSACDPSVHGALHITLSTFTYNSMLDPLVYFSSPPKFNKLIKSLKPK 300
QY 301 QPGHKTQRPPEMPISNLGRRSCISVANSFQSDGQMDPHIVEWH 346
DB 301 QPGHKTQRPPEMPISNLGRRSCISVANSFQSDGQMDPHIVEWH 346

RESULT 13

US-10-044-643-2
; Sequence 2, Application US/10044643
; Publication No. US20030195335A1

; GENERAL INFORMATION:
; APPLICANT: Majumder, Kumud
; APPLICANT: Vernet, Corine
; APPLICANT: Casman, Stacie J
; APPLICANT: Wolenc, Adam R
; APPLICANT: Spaderna, Steven K
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu S
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Baumgartner, Jason C
; APPLICANT: Gusev, Vladimir
; TITLE OF INVENTION: No. US20030195335A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-748
; CURRENT APPLICATION NUMBER: US/10/044,643
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 60/193,664
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/194,614
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/195,063
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,066
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,067
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,068
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,069
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,070
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,510
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/219,855
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 60/221,284
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/221,325
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/224,588
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/239,613
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: 60/262,508
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/263,604
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,433
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/265,161
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-044-643-2

Query Match 100.0%; Score 1853; DB 14; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.6e-163;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNGSCCRIEGDTISQVMPPLLIIVAFVLGALNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
DB 1 MYNGSCCRIEGDTISQVMPPLLIIVAFVLGALNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
QY 61 DFLLMICLPFRDYYLRRHHWAFGDI PCRVGLFTLAMNRAGSIVFLTVVAADRYPKVVHP 120
DB 61 DFLLMICLPFRDYYLRRHHWAFGDI PCRVGLFTLAMNRAGSIVFLTVVAADRYPKVVHP 120

Qy	121	HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM	180
Db	121	HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM	180
Qy	181	FOLEFFEMPLGIILFCSEFKIVSLRRRQOLARQRMKKATRFIMVAIVPITCYLPSVSAR	240
Db	181	FOLEFFEMPLGIILFCSEFKIVSLRRRQOLARQRMKKATRFIMVAIVPITCYLPSVSAR	240
Qy	241	LYFLWTVPSSACDPSVHGALHITLSFTYNNSMLDPLVYVYFSSPSPKPFYNNKLCISLKEPK	300
Db	241	LYFLWTVPSSACDPSVHGALHITLSFTYNNSMLDPLVYVYFSSPSPKPFYNNKLCISLKEPK	300
Qy	301	QPGHSKTORPREMPTISNIGRRSCISVANSFQSDGQWDPHIVEMH	346
Db	301	QPGHSKTORPREMPTISNIGRRSCISVANSFQSDGQWDPHIVEMH	346

```

RESULT 14
US-10-296-081-3
; Sequence 3, Application US/10296081
; Publication No. US20030220477A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: THORNTON, Michael
; APPLICANT: LU, Yan
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: GRAUL, Richard
; APPLICANT: KHAN, Farrah A.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: WALIA, Navinder K.
; APPLICANT: NGUYEN, Damiel B.
; APPLICANT: YUE, Henry
; APPLICANT: HAFALIA, April
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: LAL, Preeti
; APPLICANT: REDDY, Roopa
; APPLICANT: KALLICK, Deborah A.
; APPLICANT: TANG, Y. Tom
; APPLICANT: AU-YOUNG, Janice
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0096 PCT
; CURRENT APPLICATION NUMBER: US/10/296,081
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/205,628; 60/206,222; 60/207,566; 60/208,834; 60/208,851
; PRIOR FILING DATE: 2000-05-18; 2000-05-22; 2000-05-25; 2000-06-02; 2000-06-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20030220477A1 7474846CD1
US-10-296-081-3

```

Qy	181	QLEFFMPLGLIILFCSPKIVWSLRRRQQLARQARMKKATRFIMVAIVFITCYLPSVSAR	240
Db	181	QLEFFMPLGLIILFCSPKIVWSLRRRQQLARQARMKKATRFIMVAIVFITCYLPSVSAR	240
Qy	241	LYFLWTVPSSACDSPVHGALHITLSFTYVNSMLDPLVYFSSPSPKFNKLIKISLKPK	300
Db	241	LYFLWTVPSSACDSPVHGALHITLSFTYVNSMLDPLVYFSSPSPKFNKLIKISLKPK	300
Qy	301	QPGHSKTQRPPEMPISNLGRSCISVANSFQSDGQMDPHIVEWH	346
Db	301	QPGHSKTQRPPEMPISNLGRSCISVANSFQSDGQMDPHIVEWH	346
RESULT 15			
US-10-210-172-178			
; Sequence 178, Application US/10210172			
; Publication No. US20040043928A1			
GENERAL INFORMATION:			
; APPLICANT: Kekuda, Ramesh			
; APPLICANT: Miller, Charles			
; APPLICANT: Patturajan, Meera			
; APPLICANT: Pena, Carol			
; APPLICANT: Rieger, Daniel			
; APPLICANT: Shmkeets, Richard			
; APPLICANT: Zethusen, Bryan			
; APPLICANT: Li, Li			
; APPLICANT: Ji, Weizhen			
; APPLICANT: Padigaru, Muralidhara			
; APPLICANT: Casman, Stacie			
; APPLICANT: Voss, Edward			
; APPLICANT: Boldog, Ferenc			
; APPLICANT: Gorman, Linda			
; APPLICANT: Leite, Mario			
; APPLICANT: Vernet, Corine			
; APPLICANT: Anderson, David			
; APPLICANT: Guo, Xiaojia			
; APPLICANT: Zhong, Mei			
; APPLICANT: Gerlach, Valerie			
; APPLICANT: Hjalt, Tord			
; APPLICANT: Rastelli, Luca			
; APPLICANT: Spytek, Kimberly			
; APPLICANT: Edinger, Shlomit			
; APPLICANT: Ellerman, Karen			
; APPLICANT: Malyankar, Uriel			
; APPLICANT: MacDougall, John			
; APPLICANT: Stone, David			
; APPLICANT: Alsbrook II, John			
; APPLICANT: Lepley, Denise et al.			
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,			
; FILE REFERENCE: 21402-416 A			
; CURRENT APPLICATION NUMBER: US/10/210,172			
; CURRENT FILING DATE: 2001-08-01			
; PRIOR APPLICATION NUMBER: 60/309,501			
; PRIOR FILING DATE: 2001-08-02			
; PRIOR APPLICATION NUMBER: 60/323,994			
; PRIOR FILING DATE: 2001-09-21			
; PRIOR APPLICATION NUMBER: 60/373,814			
; PRIOR FILING DATE: 2002-04-19			
; PRIOR APPLICATION NUMBER: 60/310,291			
; PRIOR FILING DATE: 2001-08-03			
; PRIOR APPLICATION NUMBER: 60/310,951			
; PRIOR FILING DATE: 2001-08-08			
; PRIOR APPLICATION NUMBER: 60/310,544			
; PRIOR FILING DATE: 2001-08-07			
; PRIOR APPLICATION NUMBER: 60/311,292			
; PRIOR FILING DATE: 2001-08-09			
; PRIOR APPLICATION NUMBER: 60/311,979			
; PRIOR FILING DATE: 2001-08-13			
; PRIOR APPLICATION NUMBER: 60/313,201			
; PRIOR FILING DATE: 2001-08-17			
; PRIOR APPLICATION NUMBER: 60/312,892			
; PRIOR FILING DATE: 2001-08-16			

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 327
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 178
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-210-172-178

```
Query Match      100.0%; Score 1853; DB 15; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.6e-163;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MYNGSCCRIEGDTISQVMPPLIIVAFVLGALGNVALCGCFPHMKTWKPSSTVYLFNLAVA 60
DB      1  MYNGSCCRIEGDTISQVMPPLIIVAFVLGALGNVALCGCFPHMKTWKPSSTVYLFNLAVA 60

QY     61  DFLLMICLPFRDYTLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVWHP 120
DB     61  DFLLMICLPFRDYTLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVWHP 120

QY    121  HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVOETAVSCSFIMESANGWHDIM 180
DB    121  HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVOETAVSCSFIMESANGWHDIM 180

QY    181  FOLEFPMPLGIILFCSFKIVWSLRRLRQQLARQARKKATREIMVVAIVFITCYLPSVSAR 240
DB    181  FOLEFPMPLGIILFCSFKIVWSLRRLRQQLARQARKKATREIMVVAIVFITCYLPSVSAR 240

QY    241  LYFLMTVPSSACDPSVHGALHITLSFTYNNMMLDPLVYVYFSSPFPKFNKLIKICSLKPK 300
DB    241  LYFLMTVPSSACDPSVHGALHITLSFTYNNMMLDPLVYVYFSSPFPKFNKLIKICSLKPK 300

QY    301  QPGHKTQRPPEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
DB    301  QPGHKTQRPPEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
```

Search completed: August 30, 2005, 18:38:12
Job time : 164 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2005, 18:23:45 ; Search time 173 Seconds
(without alignments)
1024.158 Million cell updates/sec

Title: US-10-719-692-6
Perfect score: 1853
Sequence: 1 MTNGSCCRIEGTISQVMP...ANFSQSDGQWDPHVEWH 346

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1853	100.0	346	1 GP81_HUMAN	Q9bxc0 homo sapien
2	1841	99.4	346	2 Q6NNU5	Q6nux5 homo sapien
3	1483	80.0	343	1 GP81_MOUSE	Q8ci31 mus musculus
4	883.5	47.7	263	2 Q8TDS4	Q8tds4 homo sapien
5	881.5	47.6	387	2 Q8NGE4	Q8nge4 homo sapien
6	880.5	47.5	387	1 G09B_HUMAN	P49019 homo sapien
7	868.5	46.9	360	2 Q9EP66	Q9ep66 mus musculus
8	862.5	46.5	360	2 Q8QZ39	Q8qz39 rattus norv
9	596	32.2	263	2 Q8NGV8	Q8ngv8 homo sapien
10	529	28.5	384	2 Q8NGW4	Q8ngw4 homo sapien
11	529	28.5	384	2 Q8GWP7	Q8gwp7 homo sapien
12	529	28.5	423	2 Q8TDS5	Q8tds5 homo sapien
13	450.5	24.3	319	2 Q9NQ20	Q9ng20 homo sapien
14	448.5	24.2	319	1 GP31_HUMAN	O00270 homo sapien
15	446.5	24.1	319	2 Q9JLS1	Q9jls1 mus musculus
16	375.5	20.3	309	2 Q8RS28	Q8rs28 mus musculus
17	371.5	20.0	309	1 CLT2_MOUSE	Q920a1 mus musculus
18	366.5	19.8	346	1 CLT2_HUMAN	Q9ns75 mus musculus
19	364	19.6	362	1 P2YR_CHICK	P34996 gallus gall
20	364	19.6	362	1 P2YR_MELGA	P49652 melalegris g
21	362.5	19.6	373	1 P2YR_BOVIN	P48042 bos taurus
22	362	19.5	345	1 CLT2_PIG	Q95n03 sus scrofa
23	358.5	19.3	373	1 P2YR_RAT	P49651 rattus norv
24	356.5	19.2	373	1 P2YR_CAVPO	P59902 cavia porce
25	355.5	19.2	309	1 CLT2_RAT	Q924t9 rattus norv
26	354	19.1	373	1 P2YR_HUMAN	P47900 homo sapien
27	351.5	19.0	373	1 P2YR_MOUSE	P49650 mus musculus
28	351.5	19.0	390	2 Q8QSQ4	Q8qsq4 carassius a
29	350.5	18.9	370	2 Q6NSP5	Q6nsp5 homo sapien
30	348.5	18.8	373	2 Q8BMJ5	Q8bmj5 mus musculus
31	346.5	18.7	370	1 P2Y9_HUMAN	Q99677 homo sapien

32	342.5	18.5	357	2 Q9DE05	Q9de05 raja erinac
33	341	18.4	361	2 Q90X57	Q90x57 xenopus lae
34	340.5	18.4	370	2 Q8BKK1	Q8bkk1 mus musculus
35	340	18.3	344	1 P2Y5_MOUSE	Q8bmc0 mus musculus
36	339	18.3	308	1 P2Y5_CHICK	P32250 gallus gall
37	337	18.2	339	2 Q8NS57	Q8ns57 homo sapien
38	336.5	18.2	370	2 Q8BLG2	Q8blg2 mus musculus
39	336	18.1	367	1 GP17_HUMAN	Q13304 homo sapien
40	336	18.1	390	2 Q8AXM7	Q8axm7 carassius a
41	333.5	18.0	339	2 Q6NS65	Q6ns65 mus musculus
42	330.5	17.8	383	2 Q6NV10	Q6nv10 brachydanio
43	330	17.8	347	2 Q7ZZA4	Q7zza4 brachydanio
44	329.5	17.8	380	2 Q9DQ06	Q9dq06 carassius a
45	327	17.6	309	1 GP35_HUMAN	Q9hc97 homo sapien

Nicotinic

RESULT 1 Nicotinic B3

ID GP81_HUMAN STANDARD; PRT; 346 AA.

AC Q9BXC0; DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DE Probable G protein-coupled receptor (GPR81) (FKSG80 protein)

GN Name=GPR81; Synonyms=FKSG80; OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606; RN [1]

RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

RX MEDLINE=21458557; PubMed=11574155; DOI=10.1016/S0378-1119(01)00651-5;

RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko O., RA Lewis T., Evans J.F., George S.R., O'Dowd B.F.;

RT "Discovery and mapping of ten novel G protein-coupled receptor genes.";

RL Gene 275:83-91 (2001).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=22040266; PubMed=12044878; DOI=10.1016/S0014-5793(02)02775-8;

RA Takeda S., Kadowaki S., Haga T., Takasu H., Mitaku S.;

RT "Identification of G protein-coupled receptor genes from the human genome sequence.";

RL FEBS Lett. 520:97-101 (2002).

RN [3]

RP SEQUENCE FROM N.A.

RX Wang Y.-G., Gong L.;

RT "Molecular cloning of FKSG80, a novel gene encoding a putative chemokine receptor.";

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RX Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S., RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;

RT "Genome-wide discovery and analysis of human seven transmembrane helix receptor genes.";

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Orphan receptor.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- TISSUE SPECIFICITY: Expressed in pituitary tissue. Not detected in frontal, temporal and occipital lobes of the cortex, basal forebrain, caudate nucleus, nucleus accumbens, and hippocampus.

CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/

AXOR 87

TGA 183

HGPRRBH422

```
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF411110; AAL26481.1; -
DR EMBL; AB083631; BAB9344.1; -
DR EMBL; AF345568; AAK29071.1; -
DR EMBL; AB065866; BAC06084.1; -
DR Genew; HGNC:4532; GPR81.
DR MIM; 606923; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 21 Extracellular (Potential).
FT TRANSMEM 22 42 1 (Potential).
FT DOMAIN 43 49 Cytoplasmic (Potential).
FT TRANSMEM 50 70 2 (Potential).
FT DOMAIN 71 89 Extracellular (Potential).
FT TRANSMEM 90 110 3 (Potential).
FT DOMAIN 111 130 Cytoplasmic (Potential).
FT TRANSMEM 131 151 4 (Potential).
FT DOMAIN 152 182 Extracellular (Potential).
FT TRANSMEM 183 203 5 (Potential).
FT DOMAIN 204 220 Cytoplasmic (Potential).
FT TRANSMEM 221 241 6 (Potential).
FT DOMAIN 242 261 Extracellular (Potential).
FT TRANSMEM 262 281 7 (Potential).
FT DOMAIN 282 346 Cytoplasmic (Potential).
FT DISULFID 88 165 By similarity.
FT CARBOHYD 3 3 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 346 AA; 39295 MW; E0DB114EEB3A47A5 CRC64;

Query Match 100.0%; Score 1853; DB 1; Length 346;
Best Local Similarity 100.0%; Pred. No. 1.8e-122;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNGSCCRIEGDTISQVMPPLLIIVAFVLGALNGVALCGFCFHKMTKPSVTYLFNLAVA 60
DB 1 MYNGSCCRIEGDTISQVMPPLLIIVAFVLGALNGVALCGFCFHKMTKPSVTYLFNLAVA 60

QY 61 DFLLMICLPFRDYLLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYPKVHP 120
DB 61 DFLLMICLPFRDYLLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYPKVHP 120

QY 121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180
DB 121 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIM 180

QY 181 FOLEFFMPLGIILFCSPKIVNSLRRLRRQQLARQARMKKATRFIMVVAIVFIITCYLPSVSAR 240
DB 181 FOLEFFMPLGIILFCSPKIVNSLRRLRRQQLARQARMKKATRFIMVVAIVFIITCYLPSVSAR 240

QY 241 LYFLMTVPSSACDPSVHGALHTLTFTYVNSMLDPLVYFSSPPKFNKLIKICSLKPK 300
DB 241 LYFLMTVPSSACDPSVHGALHTLTFTYVNSMLDPLVYFSSPPKFNKLIKICSLKPK 300

QY 301 QPGHKTQRPPEMPISNLGRRCISVANSFQSQSDQWDPHIVEWH 346
DB 301 QPGHKTQRPPEMPISNLGRRCISVANSFQSQSDQWDPHIVEWH 346

RESULT 2
Q6NXU5 PRELIMINARY; PRT; 346 AA.
AC Q6NXU5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE G protein-coupled receptor 81.
GN Name=GPR81;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

GP81_MOUSE
ID Q8C131; STANDARD; PRT; 343 AA.
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Probable G protein-coupled receptor GPR81.
GN Name=Gpr81;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wymshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
CC -!- FUNCTION: Orphan receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AK029064; BAC26273.1; -;
DR MGD; MGI:2441671; Gpr81.
DR InterPro; IPR000276; GPCR Rhodpsn.
DR InterPro; IPR002286; P2_purnceptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPTOR FL2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 21 Extracellular (Potential).
FT TRANSMEM 22 42 1 (Potential).
FT DOMAIN 43 49 Cytoplasmic (Potential).
FT TRANSMEM 50 70 2 (Potential).
FT DOMAIN 71 90 Extracellular (Potential).
FT TRANSMEM 91 111 3 (Potential).
FT DOMAIN 112 111 Cytoplasmic (Potential).

FT TRANSMEM 132 152 4 (Potential).
FT DOMAIN 153 182 Extracellular (Potential).
FT TRANSMEM 183 203 5 (Potential).
FT DOMAIN 204 220 Cytoplasmic (Potential).
FT TRANSMEM 221 241 6 (Potential).
FT DOMAIN 242 259 Extracellular (Potential).
FT TRANSMEM 260 280 7 (Potential).
FT DOMAIN 281 343 Cytoplasmic (Potential).
FT DISULFID 88 165 By similarity.
FT CARBOHYD 3 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 343 AA; 38927 MW; 917FA9499B2E03FD CRC64;
Query Match 80.0%; Score 1483; DB 1; Length 343;
Best Local Similarity 81.4%; Pred. No. 1.8e-96;
Matches 276; Conservative 19; Mismatches 44; Indels 0; Gaps 0;
QY 1 MYNGSCCRIGDTISQVMPPLILVAFVGLGALNGVALCGFCFHMKTWKPSTVYLENLAVA 60
Db 1 MDNGSCCLIEGEPISQVMPPLILVAFVGLGALNGVALCGFCFHMKTWKSSTIYLFNLAVA 60
QY 61 DFLMICLPFRDTDYLLRRRHAFGIPCRVGLFTLAMNRAGSIVELTVVAADRYFKVHP 120
Db 61 DELLMICLPFRDTDYLLRRRHAFGIPCRVGLFTLAMNRAGSIVELTVVAADRYFKVHP 120
QY 121 HHAVNTISTRVAAGIVCTLMALVILGTLYLLENHLCVOETAVSCSFIMESANGHMDIM 180
Db 121 HHVNAISNRNTAAATACVLTWLTIVLTGTYLLENHLCVOETAVSCSFIMESANGHMDIM 180
QY 181 FOLEFMPDILGILFCSFKIVMSLRROQLARQARKKATRTFMVAIVFITCYLPSVSAR 240
Db 181 FOLEFPLPLTILFCSVNVVMSLRROQLARQARKKATRTFMVAIVFITCYLPSVSAR 240
QY 241 LYFLMTVPSSACDPVSHGALHTITLFTVYNSMLDPLVYFYFSSPPPKFKVNLKICSLKPK 300
Db 241 LYFLMTVFTSACDPVSHGALHTITLFTVYNSMLDPLVYFYFSSPPPKFKVNLKICSLKPK 300
QY 301 QFGHSKTQRPPEMPTISNIGRSCISVANSFQSDGQWD 339
Db 301 RPGRKTRRSEMPISNIGRSCISVANSFQSDGQWD 339
RESULT 4
Q8TDS4 PRELIMINARY; PRT; 363 AA.
AC Q8TDS4;
DT 01-JUN-2002 (TRENDELrel. 21, Created)
DT 01-JUN-2002 (TRENDELrel. 21, Last sequence update)
DT 05-JUL-2004 (TRENDELrel. 27, Last annotation update)
DE G protein-coupled receptor HM74a (Seven transmembrane helix
DE receptor).
GN Name=GPCR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22513958; PubMed=12522134; DOI=10.1074/jbc.M210695200;
RA Wise A., Foord S.M., Fraser N.J., Barnes A.A., Elshourbagy N.,
RA Silbert M., Ignar D.M., Murdock P.R., Stepniwski K., Green A.,
RA Brown A.J., Dowell S.J., Szekeres P.G., Hassall D.G., Marshall F.H.,
RA Wilson S., Pike N.B.;
RT "Molecular identification of high and low affinity receptors for
RT nicotinic acid";
RL J. Biol. Chem. 278:9869-9874(2003).
RN [3]
RP SEQUENCE FROM N.A.
RA Elshourbagy N.A.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; D10923; BAA01721.1; -;
DR PIR; I69202; I69202.
DR HSSP; P34996; IDDD.
DR Genew; HGNC:16824; GPR109B.
DR MIM; 606039; -;
DR GO; GO:0005887; C: integral to plasma membrane; TAS.
DR GO; GO:0004930; F: G-protein coupled receptor activity; TAS.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin...; TAS.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR InterPro; IPR002286; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm1.1; -;
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G: integral to membrane; IDA.
DR PROSITE; PS0262; G: GTP binding; IDA.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 28 Extracellular (Potential).
FT TRANSMEM 29 50 1 (Potential).
FT DOMAIN 51 63 Cytoplasmic (Potential).
FT TRANSMEM 64 85 2 (Potential).
FT DOMAIN 86 102 Extracellular (Potential).
FT TRANSMEM 103 123 3 (Potential).
FT DOMAIN 124 142 Cytoplasmic (Potential).
FT TRANSMEM 143 163 4 (Potential).
FT DOMAIN 164 194 Extracellular (Potential).
FT TRANSMEM 195 209 5 (Potential).
FT DOMAIN 210 236 Cytoplasmic (Potential).
FT TRANSMEM 237 256 6 (Potential).
FT DOMAIN 257 273 Extracellular (Potential).
FT TRANSMEM 274 298 7 (Potential).
FT DOMAIN 299 387 Cytoplasmic (Potential).
FT DISULFID 100 177 By similarity.
SQ SEQUENCE 387 AA; 44481 MW; C244F562C2343647 CRC64;

Query Match 47.5%; Score 880.5; DB 1; Length 387;
Best Local Similarity 52.2%; Pred. No. 4.2e-54;
Matches 178; Conservative 49; Mismatches 107; Indels 7; Gaps 4;
QY 5 SCRIEGRDTSQVMPPLLIIVAFVLGALNGVALCGFCFHMKTWKSTVYLFNLAVDFLL 64
DB 17 NCCVFRDDFIKVPVGLGFLGGLGLALWIFCFHLKSWKSRIFLFLNLAVDFLL 76
QY 65 MCLPRTDYLRHRRHAFGDI PCRVGLFTLANRAGSIVFLTVVAADRYFKVHPHVA 124
DB 77 IICLPFMDYVRRSDMNFDPICRLVLFMFAMNRQSGSIIFLTVAADRYFRVHPHVA 136
QY 125 NTISTRVAGIVCTLMALVILGTVYLLLENHLCVQETAVSCSFIMESANGHWDIMFQLE 184
DB 137 NKISNNTAIIICLLMGITVGLTVHLLKKLLIQNGPANVCISFISCHTFRWEHAFLE 196
QY 185 FFMPLGIILFCSPKIVWSLRRLRQQLARQAKKATRFIMVAIVFTTCYLPVSARLYEL 244
DB 197 FLPLGLIILFCSPKIVWSLRRLRQQLARQAKKATRFIMVAIVFTTCYLPVSARLYEL 255
QY 245 WTVPSA---CD--PSVHGALHITLSFTYMSMLDPLVYFSSPPKFNKLKICS 299
DB 256 WLLHTSGTQCEVYRSDLAFFITLSFTYMSMLDPLVYFSSPPKFNKLKICS 315
QY 300 KQPGHKTQRPPEMPTISNIGRSCISVANSFQSGQWDP 340
DB 316 KMTGPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPPSP 355

RESULT 7
Q9EP66 PRELIMINARY; PRT; 360 AA.
AC Q9EP66
DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative seven transmembrane spanning receptor.
GN Name=Gpr109b; Synonyms=Puma-g, Pumag;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ, and C57BL/6;
RS Schaub A., Futterer A., Pfeiffer K.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -|- SURCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -|- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AJ300199; CAC17791.1; -;
DR EMBL; AJ300198; CAC17790.1; -;
DR MGD; MGI:193383; Gpr109b.
DR GO; GO:0016021; C: integral to membrane; IDA.
DR GO; GO:0005525; F: GTP binding; IDA.
DR GO; GO:0001614; F: purinergic nucleotide receptor activity; IDA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm1.1; -;
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G: PROTEIN RECEPTOR_F1_1; 1.
DR PROSITE; PS0262; G: PROTEIN RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 360 AA; 41400 MW; CCES2A2475777FC CRC64;
Query Match 46.9%; Score 868.5; DB 2; Length 360;
Best Local Similarity 55.6%; Pred. No. 2.8e-53;
Matches 178; Conservative 39; Mismatches 96; Indels 7; Gaps 4;
QY 3 NG-SCRIEGRDTSQVMPPLLIIVAFVLGALNGVALCGFCFHMKTWKSTVYLFNLAVAD 61
DB 11 NGKNCVCPDENIAKVPVGLGFLGGLGLALWIFCFHLKSWKSRIFLFLNLAVAD 70
QY 62 FLMLCLPRTDYLRHRRHAFGDI PCRVGLFTLANRAGSIVFLTVVAADRYFKVHPH 121
DB 71 FLIIICLPFLTDNYVHNDWRFGGIPCRVLMFLMANNRQSGSIIFLTVAADRYFRVHPH 130
QY 122 HAVNTISTRVAGIVCTLMALVILGTVYLLLENHLCVQETAVSCSFIMESANGHWDIMF 181
DB 131 HPLNKISNRTAIIICLLMGITVGLTVHLLYNNMTKNGEAYLCSFSICYNFRWHDAMF 190
QY 182 QLEFFMPLGIILFCSPKIVWSLRRLRQQLARQAKKATRFIMVAIVFTTCYLPVSARL 241
DB 191 LLEFPLGLIILFCSPKIVWSLRRLRQQLARQAKKATRFIMVAIVFTTCYLPVSARL 249
QY 242 YPLMTVPS---SACD--PSVHGALHITLSFTYMSMLDPLVYFSSPPKFNKLKICS 296
DB 250 RIFWLLKYVNRNCDIYSSVDLAPFTTILSFTYMSMLDPLVYFSSPPKFNKLKICS 309
QY 297 LKPGHKTQRPPEMPTISNIGRSCISVANSFQSGQWDP 316
DB 310 LRKKTGPDNNRSTSVELT 329
RESULT 8
Q80Z39 PRELIMINARY; PRT; 360 AA.
AC Q80Z39
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nicotinic acid receptor.
GN Name=HM74b;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.

```

RA Soga T., Kamhara M., Takasaki J., Matsumoto S., Saito T., Ohishi T.,
RA Hiwama H., Matsuo A., Matsushime H., Furuichi K.;
RT "Molecular identification of nicotinic acid receptor.";
RL Biochem. Biophys. Res. Commun. 0:0-0(2003).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
EMBL; AB103062; BAC58009.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 360 AA; 41458 MW; 975BDEBCA448A6C5 CRC64;

Query Match 46.5%; Score 862.5; DB 2; Length 360;
Best Local Similarity 54.7%; Pred. No. 7.3e-53;
Matches 175; Conservative 43; Mismatches 95; Indels 7; Gaps 4;

QY 3 NG-SCRIEGDTRISQVMPPELLIVAFVGLGNGVALCGFCFHMKTWKPSTVYLFNLAVAD 61
DB 11 NGKNCVFRDENIAKVLPPVGLGFVGLGNGLALWIFCFHLKSKWSSRIFLNLAVAD 70

QY 62 FLIMTCLPRTDYLRHWAAGDIPCRVGLFTLMMNRAGSIVFLTVVAADRYFKVHPH 121
DB 71 FLIIICLPFLTDYVQNDWRFSGIPCRVLMFLMMNRQSGIIFLTVVAADRYFRVHPH 130

QY 122 HAVNTISTRVAGIVCTLMALVILGTVLLLENHLCVQETAVSCSFIMESANGWHDIMF 181
DB 131 HFINKISNRTAAIISCLMGITIGLTVHLLYTDMMTRNGDANLCSSFSICYTFRWHDAMP 190

QY 182 QLEFFMPLGIILFCFSQVLSRRRQQLARQARMKKATRFIMVAIVFITCYLPVSARL 241
DB 191 LLEFPLGLGIILFCSGRIIWSLRQR-QNDHVKIKRAINFIMVAIVFICFLPSAVRI 249

QY 242 YFLWTVPSS---SACD--PSVGHALHITLSFTYVNSMLDPLVYFSSPFPKYNKIKCS 296
DB 250 RIFWLLYKHVNRCDIYSDVLAFFTTLSFTYVNSMLDPLVYFSSPFPNPFSTCINRC 309

QY 297 LKPKQGHKSTORPEMPS 316
DB 310 LRKRTLGPDNNRSTSVELT 329

RESULT 9
Q8NGV8 PRELIMINARY; PRT; 263 AA.
AC Q8NGV8;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Seven transmembrane helix receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Teutsumi S., Aburatani H., Asai K., Akiyama Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
EMBL; AB056562; BAC05891.1; -.
DR GO; GO:00050648; F:5(S)-hydroxyperoxy-6E,8Z,11Z,14Z-icosatetra. . .; ISS.
DR GO; GO:00050647; F:5-hydroxy-6E,8Z,11Z,14Z-icosatetraenoic aci. . .; ISS.
DR GO; GO:00050646; F:5-oxo-6E,8Z,11Z,14Z-icosatetraenoic acid bi. . .; ISS.
DR GO; GO:0004930; F:G-protein coupled receptor activity; ISS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; ISS.
DR GO; GO:0003087; P:regulation of GPCR biosynthesis; ISS.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 384 AA; 41426 MW; 1C8455FED8085F36 CRC64;

Query Match 28.5%; Score 529; DB 2; Length 384;
Best Local Similarity 39.2%; Pred. No. 2.1e-29;
Matches 115; Conservative 48; Mismatches 108; Indels 22; Gaps 7;

QY 4 GSCRIEGDTRISQVMPPELLIVAFVGLGNGVALCGFCFHMKTWKPSTVYLFNLAVADPL 63
DB 42 GPCHTSSSLVSFAFLAPLALFEVLGLVGNLALFICHTRPMTSNTVFLSVLVAADPL 101

```

```

DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR002286; P2_purnoceptor.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR01157; P2YFURNOCPTN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 263 AA; 30289 MW; F96BF023A5E1F1C1 CRC64;

Query Match 32.2%; Score 596; DB 2; Length 263;
Best Local Similarity 59.9%; Pred. No. 3e-34;
Matches 115; Conservative 23; Mismatches 54; Indels 0; Gaps 0;

QY 5 SCRIEGDTRISQVMPPELLIVAFVGLGNGVALCGFCFHMKTWKPSTVYLFNLAVADPL 64
DB 17 NCCVFRDDFIVKVLPPVGLGFIFGLGNGLALWIFCFHLKSKWSSRIFLNLAVADPL 76

QY 65 MICLPFRDYLRHWAAGDIPCRVGLFTLMMNRAGSIVFLTVVAADRYFKVHPH 124
DB 77 IICLPFLMDNVRRWDKFGDIPCLMLFMMNRQSGIIFLTVVAADRYFRVHPH 136

QY 125 NTISTRVAGIVCTLMALVILGTVLLLENHLCVQETAVSCSFIMESANGWHDIMFOLE 184
DB 137 NKISNRTAAIISCLMGITIGLTVHLLKMKMPIPDGGANLCSSFSICHTLQWHEAMFLE 196

QY 185 FPMELGIIILFCS 196
DB 197 FFLPLGIIILFCS 208

RESULT 10
Q8NGW4 PRELIMINARY; PRT; 384 AA.
AC Q8NGW4;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Seven transmembrane helix receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Teutsumi S., Aburatani H., Asai K., Akiyama Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
EMBL; AB056562; BAC05891.1; -.
DR GO; GO:00050648; F:5(S)-hydroxyperoxy-6E,8Z,11Z,14Z-icosatetra. . .; ISS.
DR GO; GO:00050647; F:5-hydroxy-6E,8Z,11Z,14Z-icosatetraenoic aci. . .; ISS.
DR GO; GO:00050646; F:5-oxo-6E,8Z,11Z,14Z-icosatetraenoic acid bi. . .; ISS.
DR GO; GO:0004930; F:G-protein coupled receptor activity; ISS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; ISS.
DR GO; GO:0003087; P:regulation of GPCR biosynthesis; ISS.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 384 AA; 41426 MW; 1C8455FED8085F36 CRC64;

Query Match 28.5%; Score 529; DB 2; Length 384;
Best Local Similarity 39.2%; Pred. No. 2.1e-29;
Matches 115; Conservative 48; Mismatches 108; Indels 22; Gaps 7;

QY 4 GSCRIEGDTRISQVMPPELLIVAFVGLGNGVALCGFCFHMKTWKPSTVYLFNLAVADPL 63
DB 42 GPCHTSSSLVSFAFLAPLALFEVLGLVGNLALFICHTRPMTSNTVFLSVLVAADPL 101

```

```
QY 64 IMICLPFRDYLLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHPHHA 123
Db 102 LISNPLRLRYDYLLHETWFRGAACKVNLFMSTNRWAFVLTALNRYLKVQPHRV 161
QY 124 VNTISRVAGVICTLWALVILGTVYLLLENHLCVQE--TAVSCSFIM----ESANGWHD 178
Db 162 LSRASVGAARVAGGLUWGI-----LLNGHLLLTFTSPGSCSLSTRVTKPSASLRWHQ 215
QY 179 IMFQLEFFMPLGIILFCSEFKIVMSLRRLRQQLARQARMKATRFIMVVAIVFITCLPSV- 237
Db 216 ALYLLEFFPLALILFAIVSIGLTIRNR-GLGQAGPQARMVLAAMVAVYTCFLPSII 274
QY 238 --SARLYFLWTVPSSA---CDPSVHGALHITLSFTYMSMLDPLVYFSSPSF 285
Db 275 FGMASWAFWLSACRSLDCTQLFHG----SLAFTYLSVLDPLVLYCFSSPNF 323

RESULT 11
Q86WP7 PRELIMINARY; PRT; 384 AA.
AC Q86WP7;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DE Putative 5-oxo-ETE G-protein coupled receptor.
QS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22495202; PubMed=12606753;
RA Jones C.E., Holden S., Tenailon L., Bhatia U., Seuwen K., Tranter P.,
RA Turner J., Kettle R., Bounhelal R., Charlton S., Nirmala N., Jarai G.,
RA Finan P.;
RT "Expression and characterization of a 5-oxo-6E,8Z,11Z,14Z-
RT eicosatetraenoic acid receptor highly expressed on human eosinophils
RT and neutrophils."
RL Mol. Pharmacol. 63:471-477(2003).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AY158687; AA017739.1; -.
DR GO; GO:0050648; P:5(S)-hydroxyperoxy-6E,8Z,11Z,14Z-icosatetra. . .; ISS.
DR GO; GO:0050647; P:5-hydroxy-6E,8Z,11Z,14Z-icosatetraenoic aci. . .; ISS.
DR GO; GO:0050646; P:5-oxo-6E,8Z,11Z,14Z-icosatetraenoic acid bi. . .; ISS.
DR GO; GO:0004930; P:G-protein coupled receptor activity; ISS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; ISS.
DR GO; GO:0030817; P:regulation of cAMP biosynthesis; ISS.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRRHODPSN.
DR PROSITE; PS00237; G PROTEIN RECP F1.1; 1.
DR PROSITE; PS0262; G PROTEIN RECP F1.2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 384 AA; 41412 MW; 0C5B35FED8085F36 CRC64;

Query Match 28.5%; Score 529; DB 2; Length 384;
Best Local Similarity 39.2%; Pred. No. 2.1e-29;
Matches 115; Conservative 48; Mismatches 108; Indels 22; Gaps 7;

QY 4 GSCCRIEGTTISQVMPPLIVAFVLGALNGVALCGFCFHKMTKPTSTVYLFNLAVADFL 63
Db 42 GPCHPTSSSLVSFAFLAPLALFEVLGLVGNLSALPFICHTIRPWTSTNTVFLVSLVAADFL 101
QY 64 IMICLPFRDYLLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHPHHA 123
Db 102 LISNPLRLRYDYLLHETWFRGAACKVNLFMSTNRWAFVLTALNRYLKVQPHRV 161
QY 124 VNTISRVAGVICTLWALVILGTVYLLLENHLCVQE--TAVSCSFIM----ESANGWHD 178
Db 162 LSRASVGAARVAGGLUWGI-----LLNGHLLLTFTSPGSCSLSTRVTKPSASLRWHQ 215
QY 179 IMFQLEFFMPLGIILFCSEFKIVMSLRRLRQQLARQARMKATRFIMVVAIVFITCLPSV- 237
```

```
Db 216 ALYLLEFFPLALILFAIVSIGLTIRNR-GLGQAGPQARMVLAAMVAVYTCFLPSII 274
QY 238 --SARLYFLWTVPSSA---CDPSVHGALHITLSFTYMSMLDPLVYFSSPSF 285
Db 275 FGMASWAFWLSACRSLDCTQLFHG----SLAFTYLSVLDPLVLYCFSSPNF 323

RESULT 12
Q8TDS5 PRELIMINARY; PRT; 423 AA.
AC Q8TDS5;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE G-protein coupled receptor TGI019.
GN Name=GPCR; Synonyms=OXER1, tgi019;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22191290; PubMed=12065583; DOI=10.1074/jbc.M203194200;
RA Hosoi T., Koguchi Y., Sugikawa E., Chikada A., Ogawa K., Tsuda N.,
RA Suto N., Tsunoda S., Taniguchi T., Ohnuki T.;
RT "Identification of a Novel Human Eicosanoid Receptor Coupled to
RT Gi/o."
RL J. Biol. Chem. 277:31459-31465 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AB083630; BAB89343.1; -.
DR EMBL; AB083055; BAC11806.2; -.
DR EMBL; BC063549; AAHG3549.1; -.
DR GO; GO:0050648; P:5(S)-hydroxyperoxy-6E,8Z,11Z,14Z-icosatetra. . .; NAS.
DR GO; GO:0050647; P:5-hydroxy-6E,8Z,11Z,14Z-icosatetraenoic aci. . .; NAS.
DR GO; GO:0050646; P:5-oxo-6E,8Z,11Z,14Z-icosatetraenoic acid bi. . .; NAS.
DR GO; GO:0004930; P:G-protein coupled receptor activity; NAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; NAS.
DR GO; GO:0030817; P:regulation of cAMP biosynthesis; IDA.
```


FT DOMAIN 241 265 Extracellular (Potential).
FT TRANSMEM 266 284 7 (Potential).
FT DOMAIN 285 319 Cytoplasmic (Potential).
FT CARBOHYD 5 N-linked (GlcNAc..). (Potential).
SQ SEQUENCE 319 AA; 35079 MW; 7A4F164CD9C969DD CRC64;
Query Match 24.2%; Score 448.5; DB 1; Length 319;
Best Local Similarity 34.0%; Pred. No. 8.1e-24;
Matches 100; Conservative 62; Mismatches 121; Indels 11; Gaps 5;
QY 7 CRIEGDTISQVNPPLLIIVAFVILGALNGVALCGFCFHMKTWKPSTVYLFNLAADVADFLMI 66
Db 6 CSAPTIVATAGVLLGLECGGLGNAVALWTFLEVRVWKPYPAYVLLNLALADLLAA 65
QY 67 CLPFRDYLLRRHWAFGDIPCRVGLFTLMMNRAGSIIVLTVAADRYFKVVPHPHAYNT 126
Db 66 CLPFLAAFYLSQAWHLGRVGCWALRFLLDLRSVGMFLAVALDRLVRLVVPRLKVN 125
QY 127 ISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANG-----WHDIMF 181
Db 126 LSPQALGVSGVLLMVALTCPLLISE--AAQNSTRCHSF-YSRADGSPFSIIWQEALS 182
QY 182 QLEFFMPLGIILFCFSFKIVMSLRRR--OOLARQARKKATRFIMVVAIVFITCYLPSVSAR 240
Db 183 CLQFVLFPGLIVFCNAGIIRALQKRLPEKQPKLQRAQALVILVVVLPALCFPCFLAR 242
QY 241 --LYFLMTVPSSACDPSVHGALHITLSFTYMNMLDPLVYFSSPSPFPKFNKL 292
Db 243 VLMHIFQNLGSCRALCAVAHSDVTGSLTYLHVSVPVYCFSSPTFRSSYERV 296
RESULT 15
Q9JLS1 PRELIMINARY; PRT; 319 AA.
AC Q9JLS1;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE G protein coupled receptor.
GN Name=Tcp10c;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99431663; PubMed=10501965;
RA Schimenti J.C.;
RT "ORFless, intronless, and mutant transcription units in the mouse t
RT complex responder (Tcr) locus.";
RL Mamm. Genome 10:969-976(1999).
DR EMBL; AF140708; AAF26668.1; -.
DR MGD; MGI:98543; Tcp10c.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G PROTEIN RECEPTOR F1.1; UNKNOWN 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW RECEPTOR.
SQ SEQUENCE 319 AA; 35551 MW; 571F6DFB485BD7C4 CRC64;

Query Match 24.1%; Score 446.5; DB 2; Length 319;
Best Local Similarity 32.5%; Pred. No. 1.1e-23;
Matches 104; Conservative 64; Mismatches 133; Indels 19; Gaps 7;
QY 7 CRIEGDTISQVNPPLLIIVAFVILGALNGVALCGFCFHMKTWKPSTVYLFNLAADVADFLMI 66
Db 6 CSAASTVETAVGTMLTLCVLGMGNVALWTFYFRLKVKPYPAYVLENLVADILLAT 65

QY 67 CLPFRDYLLRRHWAFGDIPCRVGLFTLMMNRAGSIIVLTVAADRYFKVVPHPHAYNT 126
Db 66 SVPPFAAFYLGKTKLGHMPCQLLLFLAFSCGVGVAFLMTVALDRLVHLVVPRLRVNL 125
QY 127 ISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFI----MESANGWHDIMF 181
Db 126 LSLRAANGISSLIWLLMVVLTPONLL---TCRTTQNSTECSPFYPTGKTAKATCOEVL 182
QY 182 QLEFFMPLGIILFCFSFKIVMSLRRR--OOLARQARKKATRFIMVVAIVFITCYLPSVSAR 240
Db 183 FLQVLLPGLISFCNGLIIRTLQKRLSBDKQPTIRRARVLVVAIMLLFLGLCFPLSVLTR 242
QY 241 --LYFLMTVPSSACDPSVHGALHITLSFTYMNMLDPLVYFSSPSPFPKFNKLKICSLK 298
Db 243 VLMHIFQEFKSCVQQAAMRASDIAGSLTCLHSTLSPAIYCFSPNPAFTHSYRKV-LKSLR 301
QY 299 PKQGHGSKTORPEEMPISNL 318
Db 302 GR-----RKAESPNDNL 314

Search completed: August 30, 2005, 18:33:48
Job time : 175 secs

THIS PAGE BLANK (USPTO)